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(54) PEPTIDES OF HUMAN PAPILLOMA VIRUS FOR USE IN HUMAN T CELL RESPONSE INDUCING COMPOSITIONS

PEPTIDE DES MENSCHLICHEN PAPILLOMAVIRUS ZUR VERWENDUNG IN
ZUSAMMENSETZUNGEN, DIE EINE MENSCHLICHE T-ZELLREAKTION INDUZIEREN

PEPTIDES DU VIRUS DU PAPILLOME HUMAIN UTILISABLES DANS LES COMPOSITIONS
INDUISANT UNE REACTION DES LYMPHOCYTES T CHEZ L'HOMME

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**EP-A- 0 375 555 EP-A- 0 456 197
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- **EUROPEAN JOURNAL OF CANCER vol. 28, no. 2/3, February 1992, pages 326 - 333 ANNETTE ALTMANN ET AL. 'Definition of immunogenic determinants of the human papillomavirus type 16 nucleoprotein E7'**
- **PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA. vol. 88, no. 13, 1 July 1991, WASHINGTON US pages 5887 - 5891 ROBERT W. TINDLE ET AL. 'A'**
- **JOURNAL OF VIROLOGY vol. 65, no. 9, September 1991, pages 4681 - 4690 SARAH A. COMERFORD ET AL. 'Identification of T- and B-cell epitopes of the E-7 protein of human papillomavirus type 16'**
- **PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA. vol. 89, no. 17, 1 September 1992, WASHINGTON US pages 7871 - 7875 HANS J. STAUSS ET AL. 'Induction of cytotoxic T lymphocytes with peptides in vitro: Identification of candidate T-cell epitopes in human papilloma virus'**

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Description**Field of the invention**

5 [0001] The invention is concerned with novel peptides derived from Human Papilloma Virus proteins and their use in pharmaceutical compositions for a prophylactic or therapeutic treatment of human individuals against Human Papilloma Virus-related diseases such as cervical cancer.

Background of the invention

10 [0002] Human Papilloma Viruses (HPVs) are implicated in the etiology of cervical cancer, the fifth most common cancer worldwide and the second cause of cancer-related death in women. If also other HPV-related cancers are taken into account, up to 10% of the worldwide mortality due to cancer is linked to HPVs. HPVs are double stranded circular DNA viruses of about 8 kilobases. Until now more than 60 genotypes have been described of which several are associated with cancer.

15 [0003] HPV-DNA can be found in cervical dysplastic lesions and in cervical carcinomas in which the percentage of HPV positivity increases up to 99% when the lesions progress towards malignancy. The most important HPV types associated with cervical carcinoma are HPV16 and 18 of which HPV16 alone accounts for more than 50% of the HPV positive cervical carcinomas.

20 [0004] The DNAs of several HPVs have been sequenced. The DNA open reading frames can be divided into early regions (E) and late regions (L). The E regions are coding for proteins needed for virus replication and transformation. The L regions encode viral capsid proteins. The E6 and E7 proteins are involved in the pathogenesis of HPV-induced abnormal cell proliferation and these genes are expressed in tissue or tumor cells obtained from cervical cancers associated with HPV infection.

25 [0005] In addition, the E6 and E7 genes of HPV16 and HPV18 are capable of inducing epithelial cell transformation in the cell culture without the presence of other HPV genes indicating that at least part of the stimulation of cell proliferation caused by HPV infection is due to the E6 and E7 viral proteins.

30 [0006] Cytotoxic T lymphocytes (CTL) are of crucial importance in the resistance against virus infections and the immune surveillance against virus-induced tumors (reviewed by Kast and Melfi, 1991). CTL specific for viruses or virus-induced tumors recognize short viral/protein-derived peptides, of about 9 amino acids in length, that are bound to the antigen presenting groove of major histocompatibility complex (MHC) class I molecules (reviewed by Kast and Melfi, 1991). Recently, in several virus systems vaccination with peptides recognized by antigen-specific CTL was shown to prevent lethal virus infections and to delay tumor growth in mice (reviewed by Kast and Melfi, 1991, and by Reinholdsson-Ljunggren et al., 1992).

35 [0007] We have succeeded in the identification of viral peptides that bind to the groove of MHC class I molecules by using the antigen processing defective cell line 174CEM.T2 generated and provided by P. Cresswell (see Salter and Cresswell, 1986). This cell line expresses the human MHC class I HLA-A2.1 and HLA-B5 alleles of which only the HLA-A2.1 molecules are expressed as partly empty and unstable molecules that can be stabilized on the cell surface with exogenously added peptides. If incubation with peptide results in an increase in the cell surface expression of this MHC molecule, this implies that the peptide binds to the groove of the HLA-A2.1 molecule and is therefore a possible candidate to be recognized by CTL. The HLA-A2.1 molecule is the most frequent HLA molecule present in the Western European Caucasoid population. About 50% of this population expresses this allele.

40 [0008] Using the amino acid sequence of the E6 and E7 proteins of HPV16 and HPV18 (Seedorf et al., 1985 see also Altmann et al. Eur. J. Cancer vol. 23, No 213, pp. 326-333 (1992); Camerford et al. J. Virol. vol. 65, N° 9, pp. 4681-4690 (1991); Tindle et al. Proc. Natl. Acad. Sci. USA vol. 88, pp. 5887-5891 (1991)) we generated all possible nonapeptides (i.e. 9 amino acid long peptides) overspanning the entire E6 and E7 region. Every amino acid was used as a start amino acid for these 9-mer peptides. Every peptide was subjected individually to the above test to determine its capacity to bind to the HLA-A2.1 molecule. With respect to HPV16, we identified in total 10 peptides in the HPV16 E6 region and 8 in the HPV16 E7 region which bound to the HLA-A2.1 molecule in the above test. With respect to HPV18, in total 9 peptides in the HPV18 E6 region and 5 in the HPV18 E7 region were identified in the above test to bind to the HLA-A2.1 molecule. This implies that important candidate peptides of HPV16 and HPV18 for use as a vaccine in HLA-A2.1 positive humans have been identified.

45 [0009] By using a second approach, we succeeded to expand the list of HLA-A2.1 binding HPV peptides a little further and to determine HPV16 E6 and E7 peptides binding to other HLA molecules, viz. to the HLA-A1, HLA-A3.2, HLA-A11.2 and HLA-A24 molecules. Said second approach consisted of a competitive immunochemical peptide-MHC binding assay using purified class I molecules and radiolabeled consensus peptides.

Summary of the invention

[0010] An object of the present invention is to provide synthetic peptides which can be used for prevention, prophylaxis, therapy and treatment of cervical carcinoma and/or adenoma and other HPV-related, in particular HPV16- and/or HPV18-related diseases.

[0011] A further object of the present invention is to provide pharmaceutical compositions which can be used for prevention, prophylaxis, therapy and treatment of cervical carcinoma and/or adenoma and other HPV-related, in particular HPV16- and/or HPV18-related diseases.

[0012] This invention provides a peptide comprising an amino acid sequence derived from a protein of human papilloma virus (HPV), wherein said amino acid sequence has the ability to bind to a human Major Histocompatibility Complex (MHC) Class I molecule.

[0013] The present invention also provides specific peptides derived from the amino acid sequence of the E6 and E7 regions of HPV16 and HPV18 which, because of their capability to bind to HLA molecules, such as e.g. the HLA-A2.1, HLA-A1, HLA-A3.2, HLA-A11.2 or HLA-A24 protein, are candidate peptides to be included in human vaccines that can induce protective or therapeutic T cell responses against HPV16 and/or HPV18.

[0014] The novel peptides of the present invention are useful in pharmaceutical compositions, as screening tools and in the prevention, prophylaxis, therapy and treatment of HPV16- and/or HPV18-induced diseases or other conditions which would benefit from inhibition of HPV16 and/or HPV18 infection.

[0015] In a preferred embodiment of the invention, said amino acid sequence is derived from protein E6 or E7 of HPV16. In another preferred embodiment of the invention, said amino acid sequence is derived from protein E6 or E7 of HPV18.

[0016] Preferably, said amino acid sequence has the ability to bind to human MHC Class I allele HLA-A2.1.

[0017] More specifically, this invention provides a peptide comprising an amino acid sequence derived from protein E6 or E7 of HPV16, wherein said amino acid sequence has the ability to bind to human MHC Class I allele HLA-A2.1 and is selected from the group consisting of:

	AMFQDPQER	(residues 7- 15 of HPV16 protein E6)
	KLPQLCTEL	(residues 18- 26 of HPV16 protein E6)
	QLCTELQTT	(residues 21- 29 of HPV16 protein E6)
	LCTELQTTI	(residues 22- 30 of HPV16 protein E6)
	ELQTTIHDI	(residues 25- 33 of HPV16 protein E6)
	LQTTIHDI	(residues 26- 34 of HPV16 protein E6)
	TIHDIILEC	(residues 29- 37 of HPV16 protein E6)
	IHDIIILECV	(residues 30- 38 of HPV16 protein E6)
	CVYCKQQLL	(residues 37- 45 of HPV16 protein E6)
	FAFRDLCIV	(residues 52- 60 of HPV16 protein E6)
	KISEYRHYC	(residues 79- 87 of HPV16 protein E6)
	PLCDLLIRC	(residues 102-110 of HPV16 protein E6)
	TLHEYMLDL	(residues 7- 15 of HPV16 protein E7)
	YMLDLQPET	(residues 11- 19 of HPV16 protein E7)
	MLDLQPETT	(residues 12- 20 of HPV16 protein E7)
	RLCVQSTHV	(residues 66- 74 of HPV16 protein E7)
	TLEDLLMGT	(residues 78- 86 of HPV16 protein E7)
	LLMGTLGIV	(residues 82- 90 of HPV16 protein E7)
	GTLGIVCPI	(residues 85- 93 of HPV16 protein E7)
	TLGIVCPIC	(residues 86- 94 of HPV16 protein E7), and

[0018] a fragment, homolog, isoform, derivative, genetic variant or conservative variant of any one of these amino acid sequences which has the ability to bind to human MHC Class I allele HLA-A2.1.

[0019] More specifically, this invention provides a peptide comprising an amino acid sequence derived from protein E6 or E7 of HPV18, wherein said amino acid sequence has the ability to bind to human MHC Class I allele HLA-A2.1 and is selected from the group consisting of:

KLPDLCTEL	(residues 13- 21 of HPV18 protein E6)
SLQDIEITC	(residues 24- 32 of HPV18 protein E6)

(continued)

5	LQDIEITCV EITCVYCKT KTVLELTEV ELTEVFEFA FAFKDLFVV DTLEKLNTT LTNTGLYNL TLQDIVLHL FQQQLFLNLT QLFLNLTLSF LFLNLTLSFV LSFVCPWCA	(residues 25- 33 of HPV18 protein E6) (residues 29- 37 of HPV18 protein E6) (residues 36- 44 of HPV18 protein E6) (residues 40- 48 of HPV18 protein E6) (residues 47- 55 of HPV18 protein E6) (residues 88- 96 of HPV18 protein E6) (residues 93-101 of HPV18 protein E6) (residues 7- 15 of HPV18 protein E7) (residues 86- 94 of HPV18 protein E7) (residues 88- 96 of HPV18 protein E7) (residues 89- 97 of HPV18 protein E7) (residues 94-102 of HPV18 protein E7), and
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a fragment, homolog, isoform, derivative, genetic variant or conservative variant of any one of these amino acid sequences which has the ability to bind to human MHC Class I allele HLAA2.1.

[0019] According to another preferred embodiment of this invention, said amino acid sequence has the ability to bind to human MHC Class I allele HLA-A1.

[0020] More specifically, this invention provides a peptide comprising an amino acid sequence derived from protein E6 or E7 of HPV16, wherein said amino acid sequence has the ability to bind to human MHC Class I allele HLA-A1 and is selected from the group consisting of:

25	YRDGNPYAV WTGRCMSCC MSCCRSSRT TTDLYCYEQ EIDGPAGQA HVDIRTLED	(residues 61- 69 of HPV16 protein E6) (residues 139-147 of HPV16 protein E6) (residues 144-152 of HPV16 protein E6) (residues 19- 27 of HPV16 protein E7) (residues 37- 45 of HPV16 protein E7) (residues 73- 81 of HPV16 protein E7), and
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a fragment, homolog, isoform, derivative, genetic variant or conservative variant of any one of these amino acid sequences which has the ability to bind to human MHC Class I allele HLA-A1.

[0021] According to another preferred embodiment of this invention, said amino acid sequence has the ability to bind to human MHC Class I allele HLA-A3.2.

[0022] More specifically, this invention provides a peptide comprising an amino acid sequence derived from protein E6 or E7 of HPV16, wherein said amino acid sequence has the ability to bind to human MHC Class I allele HLA-A3.2 and is selected from the group consisting of:

40	AMFQDPQER IILECVYCK CVYCKQQLL VYCKQQLLR QQLLRREVY IVYRDGNPY YAVCDKCLK AVCDKCLKF VCDKCLKFY KFYSKISEY KISEYRHYC ISEYKHHCY RHYCYSLYG SLYGTTLEQ TTLEQQYNK QQYNKPLCD	(residues 7- 15 of HPV16 protein E6) (residues 33- 41 of HPV16 protein E6) (residues 37- 45 of HPV16 protein E6) (residues 38- 46 of HPV16 protein E6) (residues 42- 50 of HPV16 protein E6) (residues 59- 67 of HPV16 protein E6) (residues 67- 75 of HPV16 protein E6) (residues 68- 76 of HPV16 protein E6) (residues 69- 77 of HPV16 protein E6) (residues 75- 83 of HPV16 protein E6) (residues 79- 87 of HPV16 protein E6) (residues 80- 88 of HPV16 protein E6) (residues 84- 92 of HPV16 protein E6) (residues 89- 97 of HPV16 protein E6) (residues 93-101 of HPV16 protein E6) (residues 97-105 of HPV16 protein E6)
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(continued)

5	LIRCINCQK HLDKKQRFH CMSCCRSSR SCCRSSRTR CCRSSRTRR HYNIVTFCC YNIVTFCK CCKCDSTLR KCDSTLRLC	(residues 107-115 of HPV16 protein E6) (residues 125-133 of HPV16 protein E6) (residues 143-151 of HPV16 protein E6) (residues 145-153 of HPV16 protein E6) (residues 146-154 of HPV16 protein E6) (residues 51- 59 of HPV16 protein E7) (residues 52- 60 of HPV16 protein E7) (residues 58- 66 of HPV16 protein E7) (residues 60- 68 of HPV16 protein E7), and
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a fragment, homolog, isoform, derivative, genetic variant or conservative variant of any one of these amino acid sequences which has the ability to bind to human MHC Class I allele HLA-A3.2.

[0023] According to another preferred embodiment of this invention said amino acid sequence has the ability to bind to human MHC Class I allele HLA-A11.2.

[0024] More specifically, this invention provides a peptide comprising an amino acid sequence derived from protein E6 or E7 of HPV16, wherein said amino acid sequence has the ability to bind to human MHC Class I allele HLA-A11.2 and is selected from the group consisting of:

25	AMFQDPQER IILECVYCK CVYCKQQLL VYCKQQLLR QQLLRREVY IVYRDGNPY YAVCDKCLK AVCDKCLKF VCDKCLKFY KISEYRHYC ISEYRHYCY LIRCINCQK TGRCMSCCR CMSCCRSSR SCCRSSRTR HYNIVTFCC YNIVTFCK CCKCDSTLR VCPICSQKP	(residues 7- 15 of HPV16 protein E6) (residues 33- 41 of HPV16 protein E6) (residues 37- 45 of HPV16 protein E6) (residues 38- 46 of HPV16 protein E6) (residues 42- 50 of HPV16 protein E6) (residues 59- 67 of HPV16 protein E6) (residues 67- 75 of HPV16 protein E6) (residues 68- 76 of HPV16 protein E6) (residues 69- 77 of HPV16 protein E6) (residues 79- 87 of HPV16 protein E6) (residues 80- 88 of HPV16 protein E6) (residues 107-115 of HPV16 protein E6) (residues 140-148 of HPV16 protein E6) (residues 143-151 of HPV16 protein E6) (residues 145-153 of HPV16 protein E6) (residues 51- 59 of HPV16 protein E7) (residues 52- 60 of HPV16 protein E7) (residues 58- 66 of HPV16 protein E7) (residues 90- 98 of HPV16 protein E7), and
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a fragment, homolog, isoform, derivative, genetic variant or conservative variant of any one of these amino acid sequences which has the ability to bind to human MHC Class I allele HLA-A11.2.

[0025] According to another preferred embodiment of this invention, said amino acid sequence has the ability to bind to human MHC Class I allele HLA-A24.

[0026] More specifically, this invention provides a peptide comprising an amino acid sequence derived from protein E6 or E7 of HPV16, wherein said amino acid sequence has the ability to bind to human MHC Class I allele HLA-A24 and is selected from the group consisting of:

55	MHQKRTAMF LQTTHDII VYCKQQLLR LLRREVYDF VYDFAFRDL PYAVCDKCL	(residues 1- 9 of HPV16 protein E6) (residues 26- 34 of HPV16 protein E6) (residues 38- 46 of HPV16 protein E6) (residues 44- 52 of HPV16 protein E6) (residues 49- 57 of HPV16 protein E6) (residues 66- 74 of HPV16 protein E6)
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(continued)

KCLKFYSKI	(residues 72- 80 of HPV16 protein E6)
EYRHHCYSL	(residues 82- 90 of HPV16 protein E6)
HYCYSLYGT	(residues 85- 93 of HPV16 protein E6)
CYSLYGTTL	(residues 87- 95 of HPV16 protein E6)
RFHMIRGRW	(residues 131-139 of HPV16 protein E6)
RAHYNIVTF	(residues 49- 57 of HPV16 protein E7), and

10 a fragment, homolog, isoform, derivative, genetic variant or conservative variant of any one of these amino acid sequences which has the ability to bind to human MHC Class I allele HLA-A24.

15 [0027] This invention further provides a pharmaceutical composition containing a prophylactically or therapeutically effective amount of a peptide according to the invention, and a pharmaceutically acceptable carrier, diluent, excipient or adjuvant. Preferably, said pharmaceutical composition contains a peptide according to the invention which is able to induce a T cell response effective against HPV, in particular a HLA class I-restricted CD8⁺ cytotoxic T cell response.

Brief description of the drawings

20 [0028] Figure 1 gives the result of binding analyses of 240 HPV16 E6 and E7 nonapeptides to HLA-A2.1 expressed on 174CEM.T2 cells. Background fluorescence level (without adding peptides) was set on an arbitrary mean fluorescence level of 70. Binding of a peptide was regarded positive when twice the level of background fluorescence was reached. The 18 binding peptides are numbered 1 to 18; this numbering corresponds to the numbering in Table I.

25 [0029] Figure 2 gives the result of binding analyses of 247 HPV18 E6 and E7 nonapeptides to HLA-A2.1 expressed on 174CEM.T2 cells. Background fluorescence level (without adding peptides) was set on an arbitrary mean fluorescence level of 70. Binding of a peptide was regarded positive when twice the level of background fluorescence was reached. The 14 binding peptides are numbered 1 to 14; this numbering corresponds to the numbering in Table II.

30 [0030] Figure 3 is a graph showing the primary CTL response of human lymphocytes from healthy donor blood against an HPV16 peptide (peptide MLQLQPETT, No. 13 in Table I, SEQ ID NO 15). Bulk = bulk culture of CTL; clone = CTL clone from limiting dilution; irr. peptide = irrelevant peptide (control); and E/T ratio = effector target ratio.

Detailed description of the invention

35 [0031] The invention is directed to peptides comprising an amino acid sequence derived from a protein of HPV, wherein said amino acid sequence has the ability to bind to a human MHC Class I molecule. In view of our own experience with other viruses, the best candidates for induction of HLA class I restricted CD8⁺ cytotoxic T cells are the strongest binding peptides.

40 [0032] A most preferred embodiment of the invention concerns peptides comprising an amino acid sequence derived from protein E6 or E7 of HPV16, wherein said amino acid sequence has the ability to bind to human MHC Class I allele HLA-A2.1. Specifically, such peptides comprise the following amino acid sequences derived from the noted regions of HPV16 (see Table I; the amino acids are identified by the one-letter code of amino acids).

TABLE I

Peptides derived from HPV16 proteins E6 and E7 binding to HLA-A2.1			
Peptide No.	Amino acid sequence	protein (region)	SEQ ID NO
-	AMFQDPQER	E6 (residues 7- 15)	1
1	KLPQLCTEL	E6 (residues 18- 26)	2
2	QLCTELQTT	E6 (residues 21- 29)	3
3	LCTELQTTI	E6 (residues 22- 30)	4
4	ELQTTIHDI	E6 (residues 25- 33)	5
5	LQTTIHDI	E6 (residues 26- 34)	6
6	TIHDIILEC	E6 (residues 29- 37)	7
7	IHDIIILECV	E6 (residues 30- 38)	8
8	CVYCKQQLL	E6 (residues 37- 45)	9
-	FAFRDLCIV	E6 (residues 52- 60)	10
9	KISEYRHYC	E6 (residues 79- 87)	11

TABLE I (continued)

Peptides derived from HPV16 proteins E6 and E7 binding to HLA-A2.1				
	Peptide No.	Amino acid sequence	protein (region)	SEQ ID NO
5 10 15	10	PLCDLLIRC	E6 (residues 102-110)	12
	11	TLHEYMLDL	E7 (residues 7 - 15)	13
	12	YMLDLQPET	E7 (residues 11 - 19)	14
	13	MLDLQPETT	E7 (residues 12 - 20)	15
	14	RLCVQSTHV	E7 (residues 66 - 74)	16
	15	TLEDLLMGT	E7 (residues 78 - 86)	17
	16	LLMGTLGIV	E7 (residues 82 - 90)	18
	17	GTLGIVCPI	E7 (residues 85 - 93)	19
	18	TLGIVCPIC	E7 (residues 86 - 94)	20

[0033] Another most preferred embodiment of the invention concerns peptides comprising an amino acid sequence derived from protein E6 or E7 of HPV18, wherein said amino acid sequence has the ability to bind to human MHC Class I allele HLA-A2.1. Specifically, such peptides comprise the following amino acid sequences derived from the noted regions of HPV18 (see Table II; the amino acids are identified by the one-letter code of amino acids).

TABLE II

Peptides derived from HPV18 proteins E6 and E7 binding to HLA-A2.1				
	Peptide No.	Amino acid sequence	protein (region)	SEQ ID NO
25 30 35 40	1	KLPDLCTEL	E6 (residues 13 - 21)	21
	2	SLQDIEITC	E6 (residues 24 - 32)	22
	3	LQDIEITCV	E6 (residues 25 - 33)	23
	4	EITCVYCKT	E6 (residues 29 - 37)	24
	5	KTVLELTTEV	E6 (residues 36 - 44)	25
	6	ELTEVFEFA	E6 (residues 40 - 48)	26
	7	FAFKDLFVV	E6 (residues 47 - 55)	27
	8	DTLEKLTNT	E6 (residues 88 - 96)	28
	9	LTNTGLYNL	E6 (residues 93 - 101)	29
	10	TLQDIVLHL	E7 (residues 7 - 15)	30
	11	FQQLFLNTL	E7 (residues 86 - 94)	31
	12	QLFLNTLSF	E7 (residues 88 - 96)	32
	13	LFLNTLSFV	E7 (residues 89 - 97)	33
	14	LSFVCPWCA	E7 (residues 94 - 102)	34

[0034] Another preferred embodiment of the invention concerns peptides comprising an amino acid sequence derived from protein E6 or E7 of HPV16, wherein said amino acid sequence has the ability to bind to human MHC Class I allele HLA-A1. Specifically, such peptides comprise the following amino acid sequences derived from the noted regions of HPV16 (see Table III; the amino acids are identified by the one-letter code of amino acids).

TABLE III

Peptides derived from HPV16 proteins E6 and E7 binding to HLA-A1			
	Amino acid sequence	protein (region)	SEQ ID NO
50 55	YRDGNPYAV	E6 (residues 61- 69)	35
	WTGRCMSCC	E6 (residues 139-147)	36
	MSCCRSSRT	E6 (residues 144-152)	37
	TTDLYCYEQ	E7 (residues 19- 27)	38
	EIDGPAGQA	E7 (residues 37- 45)	39
	HVDIRTLED	E7 (residues 73- 81)	40

[0035] Another preferred embodiment of the invention concerns peptides comprising an amino acid sequence derived from protein E6 or E7 of HPV16, wherein said amino acid sequence has the ability to bind to human MHC Class I allele HLA-A3.2. Specifically, such peptides comprise the following amino acid sequences derived from the noted regions of HPV16 (see Table IV; the amino acids are identified by the one-letter code of amino acids).

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TABLE IV

Peptides derived from HPV16 proteins E6 and E7 binding to HLA-A3.2			
	Amino acid sequence	protein (region)	SEQ ID NO
10	AMFQDPQER	E6 (residues 7- 15)	1
	IILECVYCK	E6 (residues 33- 41)	41
	CVYCKQQQLL	E6 (residues 37- 45)	9
	VYCKQQQLR	E6 (residues 38- 46)	42
	QQLLRREVY	E6 (residues 42- 50)	43
	IVYRDGNPY	E6 (residues 59- 67)	44
	YAVCDKCLK	E6 (residues 67- 75)	45
	AVCDKCLKF	E6 (residues 68- 76)	46
	VCDKCLKFY	E6 (residues 69- 77)	47
	KFYSKISEY	E6 (residues 75- 83)	48
15	KISEYRHYC	E6 (residues 79- 87)	11
	ISEYRHHCY	E6 (residues 80- 88)	49
	RHYCYSLYG	E6 (residues 84- 92)	50
	SLYGTTLEQ	E6 (residues 89- 97)	51
	TTLEQQYNK	E6 (residues 93-101)	52
	QQYNKPLCD	E6 (residues 97-105)	53
	LIRCINCQK	E6 (residues 107-115)	54
	HLDKKQRFH	E6 (residues 125-133)	55
	CMSCCRSSLR	E6 (residues 143-151)	56
	SCCRSSRTR	E6 (residues 145-153)	57
20	CCRSSRTRR	E6 (residues 146-154)	58
	HYNIVTFCC	E7 (residues 51- 59)	59
	YNIVTFCCK	E7 (residues 52- 60)	60
	CCKCDSTLR	E7 (residues 58- 66)	61
	KCDSTLRLC	E7 (residues 60- 68)	62
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[0036] Another preferred embodiment of the invention concerns peptides comprising an amino acid sequence derived from protein E6 or E7 of HPV16, wherein said amino acid sequence has the ability to bind to human MHC Class I allele HLA-A11.2. Specifically, such peptides comprise the following amino acid sequences derived from the noted regions of HPV16 (see Table V; the amino acids are identified by the one-letter code of amino acids).

TABLE V

Peptides derived from HPV16 proteins E6 and E7 binding to HLA-A11.2			
	Amino acid sequence	protein (region)	SEQ ID NO
45	AMFQDPQER	E6 (residues 7 - 15)	1
	IILECVYCK	E6 (residues 33- 41)	41
	CVYCKQQQLL	E6 (residues 37- 45)	9
	VYCKQQQLR	E6 (residues 38- 46)	42
	QQLLRREVY	E6 (residues 42- 50)	43
	IVYRDGNPY	E6 (residues 59- 67)	44
	YAVCDKCLK	E6 (residues 67- 75)	45
	AVCDKCLKF	E6 (residues 68- 76)	46
	VCDKCLKFY	E6 (residues 69- 77)	47
50			
55			

TABLE V (continued)

Peptides derived from HPV16 proteins E6 and E7 binding to HLA-A11.2			
	Amino acid sequence	protein (region)	SEQ ID NO
5 10 15	KISEYRHYC	E6 (residues 79- 87)	11
	ISEYRHYCY	E6 (residues 80- 88)	49
	LIRCINCQK	E6 (residues 107-115)	54
	TGRCMSCCR	E6 (residues 140-148)	63
	CMSCCRSSR	E6 (residues 143-151)	56
	SCCRSSRTR	E6 (residues 145-153)	57
	HYNIVTFCC	E7 (residues 51- 59)	59
	YNIVTFCKK	E7 (residues 52- 60)	60
	CCKCDSTLR	E7 (residues 58- 66)	61
	VCPICSQKP	E7 (residues 90- 98)	64

[0037] Another preferred embodiment of the invention concerns peptides comprising an amino acid sequence derived from protein E6 or E7 of HPV16, wherein said amino acid sequence has the ability to bind to human MHC Class I allele HLA-A24. Specifically, such peptides comprise the following amino acid sequences derived from the noted regions of HPV16 (see Table VI; the amino acids are identified by the one-letter code of amino acids).

TABLE VI

Peptides derived from HPV16 proteins E6 and E7 binding to HLA-A24			
	Amino acid sequence	protein (region)	SEQ ID NO
25 30 35 40	MHQKRTAMF	E6 (residues 1- 9)	65
	LQTTIHDII	E6 (residues 26- 34)	6
	VYCKQQQLR	E6 (residues 38- 46)	42
	LLRREVYDF	E6 (residues 44- 52)	66
	VYDFAFRDL	E6 (residues 49- 57)	67
	PYAVCDKCL	E6 (residues 66- 74)	68
	KCLKFYFSKI	E6 (residues 72- 80)	69
	EYRHYCYSL	E6 (residues 82- 90)	70
	HYCYSLYGT	E6 (residues 85- 93)	71
	CYSLYGTTL	E6 (residues 87- 95)	72
45	RFHNIRGRW	E6 (residues 131-139)	73
[0038] The data suggest that the peptides mentioned above are single polypeptides of identified sequences. However, homologs, isoforms or genetic variants of these peptides may exist within or outside the cellular environment. This invention encompasses all such homologs, isoforms or genetic variants of the above peptides provided that they bind to the HLA molecule in question.	RAHYNIVTF	E7 (residues 49- 57)	74
45	[0039] Polypeptides that are homologs of the peptides specifically include those having amino acid sequences which are at least about 40% conserved in relation to the amino acid sequence set forth in Tables I-VI, preferentially at least about 60% conserved, and more preferentially at least about 75% conserved.		
50	[0040] It will be understood by one of ordinary skill in the art that other variants of the peptides shown above are included within the scope of the present invention. This particularly includes any variants that differ from the above mentioned and synthesized peptides only by conservative amino acid substitution. In particular, replacements of C (cysteine) by A (alanine), S (serine), α -aminobutyric acid and others are included as it is known that cysteine-containing peptides are susceptible to (air) oxidation during synthesis and handling. Many such conservative amino acid substitutions are set forth as sets by Taylor (1986).		
55	[0041] Herein the peptides shown above or fragments thereof include any variation in the amino acid sequence, whether by conservative amino acid substitution, deletion, or other processes, provided that the polypeptides bind to the HLA molecule in question. The fragments of the peptides may be small peptides with sequences of as little as five or more amino acids, said sequences being those disclosed in Tables I-VI when said polypeptides bind to the HLA molecule in question.		

[0042] Polypeptides larger than the peptides shown are especially included within the scope of the present invention when said polypeptides induce a HPV16- or HPV18-specific CTL response in appropriate individuals (e.g. HLA-A2.1 positive individuals in the case of HLA-A2.1 binding peptides) and include a (partial) amino acid sequence as set forth in Tables I-VI, or conservative substitutions thereof. Such polypeptides may have a length up to about 30 amino acids, 5 preferably up to about 27 amino acids. Most preferably, however, the peptides have a length of from 9 to 12, more preferably 9 to 11 or even 9 to 10 amino acids, most of all preferably exactly 9 amino acids.

[0043] This invention includes the use of polypeptides generated by every means, whether genetic engineering, peptide synthesis with solid phase techniques or others. The foregoing peptides may have various chemical modifications made at the terminal ends and still be within the scope the present invention. Also other chemical modifications 10 are possible, particularly cyclic and dimeric configurations. The term "derivatives" intends to cover all such modified peptides.

[0044] The polypeptides of the present invention find utility for the treatment or prevention of diseases involving HPV16 or HPV18 such as genital warts, cervical cancer or others that are linked to HPV16 or HPV18.

[0045] For all applications the peptides are administered in an immunogenic form. Since the peptides are relatively 15 short, this may necessitate conjugation with an immunogenicity conferring carrier material such as lipids or others or the use of adjuvants.

[0046] The magnitude of a prophylactic or a therapeutic dose of polypeptides of this invention will, of course, vary 20 with the group of patients (age, sex, weight, etcetera), the nature of the severity of the condition to be treated, the particular polypeptide of this invention and its route of administration. Any suitable route of administration may be employed to achieve an effective dosage of a polypeptide identified by this invention, as well as any dosage form well known in the art of pharmacy. In addition the polypeptides may also be administered by controlled release means and/or delivery devices. They may also be administered in combination with other active substances, such as in particular, T-cell activating agents like interleukine-2 etc.

[0047] The peptides of this invention may also be useful for other purposes, such as diagnostic use. For example, 25 they may be used to check whether a vaccination with a peptide according to the invention has been successful. This may be done in vitro by testing whether said peptide is able to activate T cells of the vaccinated person.

[0048] The following examples illustrate the present invention without limiting the same thereto.

EXAMPLE 1

Materials

[0049]

35 Peptide synthesizer:

Abimed AMS 422 (Abimed Analysen-Technik GmbH, Langenfeld, Germany).

Synthesis polymer:

Tentagel S AC (0.17-0.24 meq/g, Rapp Polymere, Tübingen, Germany).

40 HPLC equipment:

The HPLC system used for analysis and purification of peptides consisted of: autosampler 2157, HPLC pump 2248, variable wavelength monitor VWM 2141, column oven 2155, low pressure mixer, all of Pharmacia Nederland B.V., Woerden, The Netherlands, a Star LC-20 dot matrix printer, Star Micronics Co., Ltd., all parts controlled by a Tandon PCAs1/386sx computer, Tandon Computer Benelux B.V., Amsterdam, The Netherlands.

45 Lyophylizer:

Virtis Centry, The Virtis Company, Inc., Gardiner (NY), USA, equipped with an Alcatel 350C vacuumpump, Alcatel CIT, Malakoff, France, connected to a Christ Alpha RVC vacuo-spin, Martin Christ Gefriertrocknungsanlagen GmbH, Osterode am Harz, Germany.

Centrifuge:

MSE Mistral 6L, Beun de Ronde, Abcoude, The Netherlands.

50 Mass spectrometer:

Bioion plasma desorption mass spectrometer (PDMS), Applied Biosystems, Inc., Foster City (CA), USA.

Amino acid Analysis:

HP Aminoquant, Hewlett Packard, Amstelveen, The Netherlands.

55 Chemicals:

All chemicals were used without further purification unless stated otherwise.

Fmoc (9-fluorenylmethyloxycarbonyl) amino acids were of the L-configuration, bearing the following side chain protecting groups: t-Bu (tert-butyl) for Asp, Glu, Tyr, Ser and Thr; Trt (trityl) for His, Asn and Gln; Pmc

(2,2,5,7,8-pentamethylchroman-6-sulfonyl) for Arg; Boc (tert-butyloxycarbonyl) for Lys, all Novasyn and purchased from Pharmacia Nederland B.V., Woerden, The Netherlands.

5 Piperidine was purchased from Aldrich Chemie Benelux N.V., Brussels, Belgium.

BOP (benzotriazole-1-yl-oxy-tris-(dimethylamino)-phosphonium hexafluorophosphate) was obtained from Richelieu Biotechnologies, St-Hyacinthe, Canada.

N-methylmorpholin (NMM, Janssen Chimica, Tilburg, The Netherlands) was distilled from NaOH at atmospheric pressure before use.

N-methylpyrrolidone (MMP, Aldrich Chemie) was vacuum-distilled under a nitrogen atmosphere (b.p. 78-80°C, 18 mm Hg) before use.

10 Acetonitrile (HPLC-grade) was purchased from Rathburn Chemicals Ltd., Walkerburn, Scotland.

Ether (Baker Analyzed grade), pentane (Baker grade) and acetic acid (Baker Analyzed grade) were purchased from J.T. Baker B.V., Deventer, The Netherlands.

15 Ethanethiol was obtained from Fluka Chemie, Brussels, Belgium.

Dichloromethane and N,N-dimethylacetamide (DMA) were purchased from Janssen Chimica, Tilburg, The Netherlands.

Trifluoroacetic acid (TFA, z.S. grade) was obtained from Merck-Schuchardt, Hohenbrunn, Germany.

Disposables:

20 Polypropylene reaction vessels containing a PTFE filter were purchased from Abimed Analysen-Technik GmbH, Langenfeld, Germany.

All other disposables used were made of polypropylene and obtained from Sarstedt B.V., Etten-Leur, The Netherlands.

Experimental conditions:

25 All experiments were performed at room temperature unless stated otherwise. All Fmoc protected aminoacids, synthesis polymers, peptides and TFA were stored at -20°C.

Peptide synthesis

[0050] Peptides were synthesized by solid phase strategies on an automated multiple peptide synthesizer (Abimed AMS 422) (see Gausepohl and Frank, 1990; Gausepohl et al., 1990).

30 [0051] The peptides were made in various runs, in each of which 48 different peptides were synthesized simultaneously.

[0052] Tentagel S AC (Rapp et al., 1990; Sheppard and Williams, 1982), a graft polymer of polyethyleneglycol spacer arms on a polystyrene matrix, was used as a resin (40-60 mg per peptide, 10 µmol Fmoc amino acid loading).

35 [0053] Repetitive couplings were performed by adding a mixture of 90 µl 0.67 M BOP (Gausepohl et al., 1988; Castro et al., 1975) in NMP, 20 µl NMM in NMP 2/1 (v/v) and 100 µl of an 0.60 M solution of the appropriate Fmoc amino acid (Fields and Noble, 1990) in NMP (6-fold excess) to each reaction vessel. At 70% of the reaction time approximately 50 µl dichloromethane was added to each reaction vessel.

[0054] Fmoc-deprotection was performed by adding 3 times 0.8 ml of piperidine/DMA 1/4 (v/v) to each reaction vessel.

40 [0055] Coupling- and deprotection times were increased as the synthesis proceeded, starting with 30 min and 3 times 3 min respectively.

[0056] Washings after couplings and Fmoc-deprotections were done with 6 times 1.2 ml DMA. After the required sequence had been reached and the last Fmoc-protection was removed the peptidylresin was washed extensively with DMA, dichloromethane, dichloromethane/ether 1/1 (v/v) and ether respectively, and dried.

Peptide cleavage and isolation

[0057] Cleavage of the peptides from the resin and removal of the side chain protecting groups was performed by adding 6 times 200 µl TFA/water 19/1 (v/v) at 5 min intervals to each reaction vessel, thus yielding free carboxylic peptides. For Trp-containing peptides TFA/water/ethanethiol 18/1/1 (v/v/v) was used.

[0058] Two hours after the first TFA addition the peptides were precipitated from the combined filtrates by addition of 10 ml ether/pentane 1/1 (v/v) and cooling to -20°C. The peptides were isolated by centrifugation (-20°C, 2500g, 10 min).

[0059] After treatment of the pellet with ether/pentane 1/1 (v/v) and isolation by the same centrifugation procedure, the peptides were dried at 45°C for 15 min.

[0060] Each of the peptides was dissolved in 2 ml water (or 2 ml 10 vol.% acetic acid), the solution frozen in liquid nitrogen for 3 min, and lyophilized while being centrifuged (1300 rpm, 8-16 h).

Analysis and purification

[0061] The purity of the peptides was determined by reversed phase HPLC; an aliquot of about 50 nmol was dissolved in 100 µl 30 vol.% acetic acid. Of this solution 30 µl was applied to an RP-HPLC system equipped with a ternary solvent system; A: water, B: acetonitrile, C: 2 vol.% TFA in water.

[0062] Gradient elution (1.0 ml/min) was performed from 90% A, 5% B, 5% C to 20% A, 75% B, 5% C in 30 min. Detection was at 214 nm.

[0063] Samples taken at random were analysed by mass spectrometry on a PDMS. The 31 binding peptides were all analysed by mass spectrometry on a PDMS and by quantitative amino acid analysis after hydrolysis on a HP Aminoquant. Of all analysed samples the difference between calculated and measured masses was within the experimental error (0.1%) as specified by the producer of the equipment used. All aminoacid compositions were as expected.

EXAMPLE 2

Peptides

[0064] Of all 240 HPV16 peptides and 247 HPV18 peptides that had been freeze dried, 5 mg was weighed and dissolved in 1 ml of distilled water adjusted with 5N NaOH to a pH of 12. Peptides that did not readily dissolve were treated with 150 µl of 100% acetic acid glacial (CH₃COOH, Merck Darmstadt, Germany: 56-1000) after which the pH was neutralized to pH 7 with 5N NaOH diluted in distilled water (Merck Darmstadt, Germany: 6498). Peptides which still did not dissolve were treated with 100 µl of 5N NaOH to pH 12 after which the pH was neutralized to pH 7 with 10% acetic acid glacial in distilled water. Of all peptides a dilution of 1 mg/ml in 0.9% NaCl was made.

Cells

[0065] 174CEM.T2 cells were cultured in Iscove's modified Dulbecco's medium (Biochrom KG Seromed Berlin, Germany: F0465) supplemented with 100IU/ml penicillin (Biocades Pharma, Leiderdorp, The Netherlands), 100 µg/ml kanamycin (Sigma St. Louis, USA:K-0254), 2mM glutamine (ICN Biomedicals Inc. Costa Mesa, CA, USA:15-801-55) and 10% fetal calf serum (FCS, Hyclone Laboratories Inc. Logan, Utah, USA:A-1115-L). Cells were cultured at a density of 2.5 × 10⁵/ml during 3 days at 37°C, 5% CO₂ in humified air.

Peptide binding

[0066] 174CEM.T2 cells were washed twice in culture medium without FCS and put in serum-free culture medium to a density of 2 × 10⁶ cells/ml. Of this suspension 40 µl was put into a V bottomed 96 well plate (Greiner GmbH, Frickenhausen, Germany: 651101) together with 10 µl of the individual peptide dilutions (of 1 mg/ml). The end concentration is 200 µg/ml peptide with 8 × 10⁴ 174CEM.T2 cells. This solution was gently agitated for 3 minutes after which an incubation time of 16 hours at 37°C, 5% CO₂ in humified air took place. Then cells were washed once with 100 µl 0.9% NaCl, 0.5% bovine serum albumin (Sigma St. Louis, USA: A-7409), 0.02% NaN₃ (Merck Darmstadt, Germany:822335). After a centrifuge round of 1200 rpm the pellet was resuspended in 50 µl of saturating amounts of HLA-A2.1 specific mouse monoclonal antibody BB7.2 for 30 minutes at 4°C. Then cells were washed twice and incubated for 30 minutes with F(ab)₂ fragments of goat anti-mouse IgG that had been conjugated with fluoresceine isothiocyanate (Tago Inc Burlingame, CA, USA: 4350) in a dilution of 1:40 and a total volume of 25 µl.

[0067] After the last incubation, cells were washed twice and fluorescence was measured at 488 nanometer on a FACScan flow-cytometer (Becton Dickinson, Franklin Lakes, NJ, USA). The results are shown in fig. 1 (HPV16 peptides) and fig. 2 (HPV18 peptides), respectively.

[0068] The 174CEM.T2 cell line expresses "empty" and unstable HLA-A2.1 molecules that can be stabilized when a peptide is binding to the peptide presenting groove of these molecules. A stabilized HLA-A2.1 molecule that will not easily degrade is the result of binding of an analyzed peptide. This leads to an increase in cell surface expression of the HLA-A2.1 molecule.

Results

[0069] In order to identify E6 and E7 region peptides of HPV16 and HPV18 that could bind to HLA-A2.1 molecules expressed by 174CEM.T2 cells, the amino acid sequences of E6 and E7 of HPV16 and HPV18 were examined (4). Every amino acid in the E6 and E7 region was used as the first amino acid of a 9 amino acid long peptide. In this way the entire E6 and E7 regions of HPV16 and HPV18 were covered. Nine amino acid long peptides were chosen because they fit the presently known rules for length of peptides that bind to the groove of HLA-A2.1 molecules (reviewed by

Kast and Melief, 1991). For practical reasons, in a first series of experiments alanine residues were used in the tested peptides instead of the cysteine residues occurring in the natural sequence. Thereafter, a second series of experiments was carried out with peptides containing the cysteine residues of the natural sequence.

[0070] Only the peptides Nos. 1-18 of Table I and Nos. 1-14 of Table II (including those containing alanine residues instead of the cysteine residues) were able to significantly upregulate the expression of HLA-A2.1 molecules measured as mean HLA-A2.1 fluorescence of 174CEM.T2 cells indicating their binding to the HLA-A2.1 molecule as described in Example 2. None of the 222 + 233 other peptides were able to do this. The results of the fluorescence measurement are given in Tables VII and VIII and shown in Figures 1 and 2. The peptides are numbered in accordance with the numbering in Tables I and II.

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MF = Mean Fluorescence

$$FI = \text{Fluorescence Index} = \frac{(MF)_{\text{experiment}} - (MF)_{\text{blank}}}{(MF)_{\text{blank}}}$$

15

[0071] With background fluorescence level (without adding peptides) set on a Fluorescence Index level of 0, binding of a peptide was regarded positive when the level of fluorescence was ≥ 0.5 .

20

TABLE VII:

HPV16 peptides		
Peptide	FI	MF
1	1.6	168.6
2	2.2	211.9
3	0.7	113.6
4	0.6	108.0
5	1.6	170.4
6	1.8	184.5
7	1.3	150.7
8	2.0	195.0
9	2.2	211.7
10	2.1	204.8
11	1.2	144.5
12	3.3	283.9
13	2.3	217.6
14	2.8	250.0
15	1.8	182.8
16	0.8	118.8
17	2.3	216.1
18	2.5	227.8

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TABLE VIII:

HPV18 peptides		
Peptide	FI	MF
1	2.1	439.3
2	0.7	243.9
3	1.3	327.8
4	0.5	206.0
5	2.3	467.5
6	1.1	289.0
7	2.3	462.9

TABLE VIII: (continued)

HPV18 peptides		
Peptide	FI	MF
8	0.7	238.2
9	1.5	352.5
10	2.7	519.6
11	0.8	244.5
12	0.8	258.2
13	1.6	360.3
14	0.9	262.0

[0072] These experiments indicate that only a limited proportion of peptides have the ability to bind to the HLA-A2.1 molecule and are therefore the only candidates of the HPV16 and HPV18 E regions to be recognized by human CTL because CTL recognize peptides only when bound to HLA molecules.

EXAMPLE 3

[0073] This example illustrates in vitro induction of primary immune response against HPV peptides using the processing defective cell line 174CEM.T2.

[0074] The expression of HLA-A2.1 on 174CEM.T2 cells (T2) is increased by incubating T2 cells in medium containing relevant peptide. T2 cells will present the relevant peptide bound to HLA-A2.1 in high amount and therefore are good antigen presenting cells (APC). In the response inducing method described below the T2 cell line is used as APC and post-Ficoll mononuclear cells are used as responder cells.

Method

[0075]

1) Peptide loading of HLA-A2.1 on T2

T2 cells in a concentration of 2×10^6 cells per ml were incubated for 13 h at 37°C in a T 25 flask (Becton Dickinson, Falcon, Plymouth Engeland cat.nr. 3013) in serum-free IMDM (= Iscoves Modified Dulbecco's Medium: Biochrom KG, Seromed Berlin, Germany, cat.nr. F0465) with glutamine (2mM, ICN Biochemicals Inc., Costa Meisa, USA, cat.nr. 15-801-55), antibiotics (100 IU/ml penicilline (Brocades Pharma, Leiderdorp, The Netherlands, 100 µg/ml kanamycine (Sigma, St. Louis, USA, K-0245)) and the selected peptide MLQLQPETT (= JWK3; SEQ ID NO:15) in a concentration of 80 µg/ml.

2) Mitomycine C treatment of T2 (APC)

These incubated T2 cells were spun down and subsequently treated in a density of 20×10^6 cells/ml with Mitomycine C (50µg/ml) in serum-free RPMI (Gibco Paislan, Scotland, cat.nr. 041-02409) medium for 1 h at 37°C. Hereafter the T2 cells were washed three times in RPMI.

3) Preparing for primary immune response induction

All wells of a 96-well-U-bottom plate (Costar, Cambridge, USA, cat.nr. 3799) were filled with 100,000 Mitomycine C-treated T2 cells in 50µl serum-free, complete RPMI medium (glutamine (2mM, ICN Biochemicals Inc., Costa Meisa, USA, cat.nr. 15-801-55), penicilline (100 IU/ml, Brocades Pharma, Leiderdorp, The Netherlands), kanamycine (100µg/ml, Sigma, St. Louis, USA, K-0245)) and the peptide MLQLQPETT in a concentration of 80 µg/ml.

4) Responder cells

Responder cells are mononuclear peripheral blood lymphocytes (PBL) of a HLA-A2.1 subtyped donor (= C. B.). The PBL were separated from a buffy coat by Ficoll-procedure (Ficoll preparation: Lymphoprep of Nycomed-pharma, Oslo, Norway, cat.nr. 105033) and washed two times in RPMI. After separation and washing, the PBL were resuspended in complete RPMI medium with 30% human pooled serum (HPS) (HPS is tested for suppression activity in Mixed Lymphocyte Cultures).

5) Incubation of primary immune response

400,000 PBL-C.B. in 50µl of medium (the medium described in header 4) were added to each well of the 96-well-U-bottom plate already filled with T2 cells and cultured for 7 days at 37°C in an incubator with 5% CO₂ and 90% humidity.

5 6) Restimulation (day 7)

On day 7 after incubation of PBL, peptide MLQLQPETT and T2 cells (headers 1-5), the PBL-C.B. were restimulated with peptide MLQLQPETT. For this purpose all cells and medium out of the 96 wells were harvested. Viable cells were isolated by Ficoll-procedure and washed in RPMI. In a new 96-well-U-bottom plate 50,000 of these viable cells were seeded to each well together with 50µl complete RPMI medium with 15% HPS. Per well 20,000 autologous, irradiated (3000 rad) PBL and 50,000 autologous, irradiated (10000 rad) EBV-transformed B-lymphocytes (= EBV-C.B.) were added together with 50µl of complete RPMI medium with 15% HPS and peptide MLQLQPETT in a concentration of 80µg/ml. The cells were cultured for 7 days at 37°C in an incubator with 5% CO₂ and 90% humidity.

15 7) Restimulation (day 14)

On day 14 after incubation of PBL, peptide MLQLQPETT and T2 cells (headers 1-5), the PBL-C.B. were restimulated with peptide MLQLQPETT. To do so the procedure under header 6 is repeated.

20 8) Cloning by Limiting Dilution

On day 21 after incubation of PBL, peptide MLQLQPETT and T2 cells, cells and medium out of the 96 wells were harvested. Viable cells were isolated by Ficoll-procedure and washed in complete RPMI with 15% HPS. This bulk of viable cells was cloned by Limiting Dilution. Into each well of a new 96-well-U-bottom plate (Costar, Cambridge, USA, cat. nr. 3799) 50µl complete RPMI medium with 15 % HPS was added together with 100 viable cells (= HPV16 bulk anti MLQLQPETT). For other new 96-well-U-bottom plates this was exactly repeated except for the number of cells for wells: subsequent plates contained 10, 1, or 0.3 cells per well. To all wells 20,000 pooled and irradiated (3000 rad) PBL of four different donors and 10,000 pooled and irradiated (10,000 rad) EBV-transformed B-cells of three different HLA-A2.1 donors (VU-4/ 518/JY) were added together with 50µl of complete RPMI medium with 15% HPS and peptide MLQLQPETT in a concentration of 40µg/ml, Leucoagglutinin in a concentration of 2% (Pharmacia, Uppsala, Sweden, cat.nr. 17-063-01), human recombinant IL-2 in a concentration of 120 IU/ml (Eurocetus, Amsterdam, The Netherlands).

30 9) Expand clones

Add per well, in a final volume of 100 µl =>

- 35 - 25,000 viable cells
 - 20,000 irradiated PBL-pool (as in header 8)
 - 10,000 irradiated EBV-pool (as in header 8)
 - 2 µg peptide MLQLQPETT
 - 6 IU recombinant IL-2.

40 [0076] On day 49 a cytotoxicity assay was performed with 65 clones and one bulk as effector cells and T2 (with or without the relevant peptide MLQLQPETT) as target cells. Background killing is defined as killing of T2 cells incubated with an irrelevant (but HLA-A2.1 binding) peptide: ATELQTTIH.

[0077] The HPV16 bulk (C.B.) anti MLQLQPETT seemed to be specific for killing MLQLQPETT -sensitized T2 cells. All the clones were not specific.

[0078] A new limiting dilution was done with the HPV16 bulk (C.B.) anti MLQLQPETT cells (as in header 8+9).

[0079] On day 28 after the new limiting dilution a cytotoxicity assay was performed with five clones (ID10, ID12, ID19, ID26, ID92) and one bulk. A representative clone is shown in fig. 3.

50 EXAMPLE 4

[0080] This example illustrates an immunochemical peptide-MHC binding assay which was used to determine which HPV16 protein E6 and E7 peptides bind to HLA-A1, A2.1, A3.2, A11.2 and A24 molecules.

[0081] The method utilizes purified class I molecules and radiolabeled synthetic probes based on consensus peptides. Competitor peptides tested for their binding to the class I molecules compete for this binding with the radiolabeled consensus peptides. The HLA-A1, A2.1, A3.2, A11.2, and A24 molecules were isolated from the following cell lines, respectively: the EBV (Eppstein Barr Virus) transformed cell line Steinlin, the EBV transformed cell line JY, the EBV transformed cell line GM3107, the cell line BVR and the EBV transformed cell line KT3. After large scale culture, cells

were lysed in NP40 (Fluka Biochemika, Buchs, Switzerland) and the lysate was passed over two pre-columns of inactivated sepharose CL 4B and Prot A Sepharose. Class I molecules were then purified from the cell lysate by affinity chromatography using Prot A Sepharose beads conjugated with B2.23.2 (anti-HLA-B and HLA-C) and anti-human HLA. The lysate was first depleted of B and C molecules by repeated passage over the B2.23.2 column. Remaining HLA-A molecules were then captured by the W6/32 column and eluted by pH 11.5 DEA/1% OG neutralized with 1 mM Tris pH 6.8 and concentrated by ultrafiltration on Amicon 30 K_D cartridges.

[0082] For binding assays, MHC amounts that resulted in binding of 15% of the radiolabeled synthetic probes (normally in the 10-50 nM range) were incubated in 0.05% NP40-PBS with about 5 nM of radiolabeled peptides and titrated amounts of unlabeled competitor peptides to be tested (usually in the 10 mg to 1 ng/ml range) in the presence of 1 µM β2M and a cocktail of protease inhibitors (with final concentrations of 1 mM PMSF, 1.3 mM 1,10-Phenanthroline, 73 µM Pepstatin A, 8 mM EDTA, 200 µM N-α-p-tosyl-L-Lysine Chloromethyl ketone). After two days at 23°C the percent of MHC-bound radioactivity was measured by size exclusion chromatography on a TSK2000 gel filtration as described by Sette et al. (1992).

[0083] Probe peptides were iodinated by using the Chloramine T method described by Buus et al. (1987). The sequences of the probe peptides used for the aforementioned HLA molecules were YLEPAIAKY for A1, FLPSDYFPSV for A2.1, KVFPYALINK for A3.2, AVDLYHFLK for A11.2, and AYIDNYNKF for A24.

[0084] To allow comparison of the data obtained in different experiments, a relative binding figure was calculated for each peptide by dividing the 50% inhibition dose (IC_{50}) for the positive control for inhibition of unlabeled probe peptides by the 50% inhibition doses for each tested peptide. The values of the 50% inhibition dose for the probes was: 81 nM for A1, 5 nM for A2.1, 30 nM for A3.2, 9 nM for A11.2 and 22 nM for A24.

[0085] Each competitor peptide was tested in two to four completely independent experiments. Since cysteine containing peptides are susceptible to (air) oxidation during synthesis and handling, these peptides were synthesized with an alanine instead of a cysteine. Arbitrarily, the competitor peptides were categorized as good binders, intermediate binders, weak binders and negative binders when they fell into the following ratio categories: 1.0-0.1, 0.1-0.01, 0.01-0.001, and < 0.001, respectively.

[0086] The results are shown in Tables IX to XIII.

TABLE IX:

HPV16 E6 and E7 peptides binding to HLA-A1 in immunochemical assay			
Peptide	protein (region)	SEQ ID NO	binding ratio to standard#
YRDGNPYAV	E6 (residues 61- 69)	35	0.008
WTGRCMSCC	E6 (residues 139-147)	36	0.020
MSCCRSSRT	E6 (residues 144-152)	37	0.019
TTDLYCYEQ	E7 (residues 19- 27)	38	0.023
EIDGPAGQAA	E7 (residues 37- 45)	39	0.025
HVDIRTLED	E7 (residues 73- 81)	40	0.014

The average IC_{50} value ±SE of the standard in the course of the experiments considered in this table was 81 ±30 nM.

TABLE X:

Additional HPV16 E6 and E7 peptides binding to HLA-A2.1 in immunochemical assay			
Peptide	protein (region)	SEQ ID NO	binding ratio to Standard#
AMFQDPQER	E6 (residues 7- 15)	1	0.0033
FAFRDLCIV	E6 (residues 52- 60)	10	0.3700

The average IC_{50} value ±SE of the standard in the course of the experiments considered in this table was 6 ±1 nM.

TABLE XI:

HPV16 E6 and E7 peptides binding to HLA-A3.2 in immunochemical assay			
Peptide	protein (region)	SEQ ID NO	binding ratio to standard#
AMFQDPQER	E6 (residues 7- 15)	1	0.1000

The average IC_{50} value ±SE of the standard in the course of the experiments considered in this table was 30 ±3 nM.

TABLE XI: (continued)

HPV16 E6 and E7 peptides binding to HLA-A3.2 in immunochemical assay				
	Peptide	protein (region)	SEQ ID NO	binding ratio to standard#
5	IILECVYCK	E6 (residues 33- 41)	41	1.5000
	CVYCKQQLL	E6 (residues 37- 45)	9	0.0320
	VYCKQQQLR	E6 (residues 38- 46)	42	0.0012
	QQLLRREVY	E6 (residues 42- 50)	43	0.0058
	IVYRDGNPY	E6 (residues 59- 67)	44	3.0000
	YAVCDKCLK	E6 (residues 67- 75)	45	0.0012
	AVCDKCLKF	E6 (residues 68- 76)	46	0.0056
	VCDKCLKFY	E6 (residues 69- 77)	47	0.0025
	KFYSKISEY	E6 (residues 75- 83)	48	0.0100
	KISEYRHYC	E6 (residues 79- 87)	11	0.0044
10	ISEYRHYCY	E6 (residues 80- 88)	49	0.0064
	RHYCYSLYG	E6 (residues 84- 92)	50	0.0036
	SLYGTTLEQ	E6 (residues 89- 97)	51	0.0080
	TTLEQQYNK	E6 (residues 93-101)	52	0.0780
	QQYNKPLCD	E6 (residues 97-105)	53	0.0045
	LIRCINCQK	E6 (residues 107-115)	54	3.7000
	HLDKKQRFH	E6 (residues 125-133)	55	0.4400
	CMSCCRSSLR	E6 (residues 143-151)	56	0.1800
	SCCRSSRSTR	E6 (residues 145-153)	57	0.0200
	CCRSSRTRR	E6 (residues 146-154)	58	0.0020
15	HYNIVTFCC	E7 (residues 51- 59)	59	0.0260
	YNIVTFCCCK	E7 (residues 52- 60)	60	0.0067
	CCKCDSTLR	E7 (residues 58- 66)	61	0.0016
	KCDSTLRLC	E7 (residues 60- 68)	62	0.0012
20				
25				
30				

The average IC₅₀ value ±SE of the standard in the course of the experiments considered in this table was 30 ±3 nM.

TABLE XII:

HPV16 E6 and E7 peptides binding to HLA-A11.2 in immunochemical assay				
	Peptide	protein (region)	SEQ ID NO	binding ratio to standard#
35	AMFQDPQPER	E6 (residues 7- 15)	1	0.8400
	IILECVYCK	E6 (residues 33- 41)	41	6.7000
	CVYCKQQLL	E6 (residues 37- 45)	9	0.0450
	VYCKQQQLR	E6 (residues 38- 46)	42	0.0022
	QQLLRREVY	E6 (residues 42- 50)	43	0.0084
	IVYRDGNPY	E6 (residues 59- 67)	44	0.4700
	YAVCDKCLK	E6 (residues 67- 75)	45	0.0074
	AVCDKCLKF	E6 (residues 68- 76)	46	0.0037
	VCDKCLKFY	E6 (residues 69- 77)	47	0.0030
	KISEYRHYC	E6 (residues 79- 87)	11	0.0076
40	ISEYRHYCY	E6 (residues 80- 88)	49	0.4300
	LIRCINCQK	E6 (residues 107-115)	54	0.0120
	TGRCMSSCR	E6 (residues 140-148)	63	0.0012
	CMSCCRSSLR	E6 (residues 143-151)	56	0.0084
	SCCRSSRSTR	E6 (residues 145-153)	57	0.0330
	HYNIVTFCC	E6 (residues 51- 59)	59"	0.0010
45				
50				
55				

The average IC₅₀ value ±SE of the standard in the course of the experiments considered in this table was 10 ±3 nM.

TABLE XII: (continued)

HPV16 E6 and E7 peptides binding to HLA-A11.2 in immunochemical assay			
Peptide	protein (region)	SEQ ID NO	binding ratio to standard#
YNIVTFCCCK	E7 (residues 52- 60)	60	0.0060
CCKCDSTLR	E7 (residues 58- 66)	61	0.0110
VCPICSQKP	E7 (residues 90- 98)	64	0.0012

The average IC₅₀ value ±SE of the standard in the course of the experiments considered in this table was 10 ±3 nM.

10

TABLE XIII:

HPV16 E6 and E7 peptides binding to HLA-A24 in immunochemical assay			
Peptide	protein (region)	SEQ ID NO	binding ratio to standard#
MHQKRTAMF	E6 (residues 1- 9)	65	0.0049
LQTTIHDII	E6 (residues 26- 34)	6	0.0200
VYCKQQQLLR	E6 (residues 38- 46)	42	0.0011
LLRREVYDF	E6 (residues 44- 52)	66	0.0023
VYDFAFRDL	E6 (residues 49- 57)	67	0.0610
PYAVCDKCL	E6 (residues 66- 74)	68	0.0055
KCLKFYSKI	E6 (residues 72- 80)	69	0.1100
EYRHYCYSL	E6 (residues 82- 90)	70	0.0460
HYCYSLYGT	E6 (residues 85- 93)	71	0.0037
CYSLYGTTL	E6 (residues 87- 95)	72	0.1200
RFHNIRGRW	E6 (residues 131-139)	73	0.1000
RAHYNIVTF	E7 (residues 49- 57)	74	0.0670

The average IC₅₀ value ±SE of the standard in the course of the experiments considered in this table was 22 ±6 nM.

30

References:

[0087]

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peptide interactions. J. Immunol. 148: 844 (1992)

14. S. Buus, A. Sette, S.M. Colon, C. Miles and H.M. Grey. The relation between major histocompatibility complex (MHC) restriction and the capacity of Ia to bind immunogenic peptides. Science 235: 1352 (1987)

5 SEQUENCE LISTING

[0088]

SEQ ID NO:1

SEQUENCE TYPE: amino acid

SEQUENCE LENGTH: 9 amino acids

AlaMetPheGlnAspProGlnGluArg
1 5 9

15

SEQ ID NO:2

SEQUENCE TYPE: amino acid

SEQUENCE LENGTH: 9 amino acids

20

LysLeuProGlnLeuCysThrGluLeu
1 5 9

25

SEQ ID NO:3

SEQUENCE TYPE: amino acid

SEQUENCE LENGTH: 9 amino acids

30

GlnLeuCysThrGluLeuGlnThrThr
1 5 9

SEQ ID NO:4

SEQUENCE TYPE: amino acid

35

SEQUENCE LENGTH: 9 amino acids

LeuCysThrGluLeuGlnThrThrIle
1 5 9

40

SEQ ID NO:5

SEQUENCE TYPE: amino acid

SEQUENCE LENGTH: 9 amino acids

45

GluLeuGlnThrThrIleHisAspIle
1 5 9

50

SEQ ID NO:6

SEQUENCE TYPE: amino acid

SEQUENCE LENGTH: 9 amino acids

55

LeuGlnThrThrIleHisAspIleIle
1 5 9

SEQ ID NO:7

SEQUENCE TYPE: amino acid

SEQUENCE LENGTH: 9 amino acids

5 **ThrIleHisAspIleIleLeuGluCys**
 1 5 9

SEQ ID NO:8

SEQUENCE TYPE: amino acid

SEQUENCE LENGTH: 9 amino acids

10 **IleHisAspIleIleLeuGluCysVal**
 1 5 9

15 SEQ ID NO:9

SEQUENCE TYPE: amino acid

SEQUENCE LENGTH: 9 amino acids

20 **CysValTyrCysLysGlnGlnLeuLeu**
 1 5 9

SEQ ID NO:10

SEQUENCE TYPE: amino acid

SEQUENCE LENGTH: 9 amino acids

25 **PheAlaPheArgAspLeuCysIleVal**
 1 5 9

30 SEQ ID NO:11

SEQUENCE TYPE: amino acid

SEQUENCE LENGTH: 9 amino acids

35 **LysIleSerGluTyrArgHisTyrCys**
 1 5 9

40 SEQ ID NO:12

SEQUENCE TYPE: amino acid

SEQUENCE LENGTH: 9 amino acids

45 **ProLeuCysAspLeuLeuIleArgCys**
 1 5 9

50 SEQ ID NO:13

SEQUENCE TYPE: amino acid

SEQUENCE LENGTH: 9 amino acids

55 ~
 ThrLeuHisGluTyrMetLeuAspLeu
 1 5 9

SEQ ID NO:14

SEQUENCE TYPE: amino acid

SEQUENCE LENGTH: 9 amino acids

5 **TyrMetLeuAspLeuGlnProGluThr**
 1 5 9

SEQ ID NO:15
SEQUENCE TYPE: amino acid
SEQUENCE LENGTH: 9 amino acids

10 **MetLeuAspLeuGlnProGluThrThr**
 1 5 9

SEQ ID NO:16
SEQUENCE TYPE: amino acid
SEQUENCE LENGTH: 9 amino acids

15 **ArgLeuCysValGlnSerThrHisVal**
 1 5 9

20 SEQ ID NO:17
SEQUENCE TYPE: amino acid
SEQUENCE LENGTH: 9 amino acids

25 **ThrLeuGluAspLeuLeuMetGlyThr**
 1 5 9

30 SEQ ID NO:18
SEQUENCE TYPE: amino acid
SEQUENCE LENGTH: 9 amino acids

35 **LeuLeuMetGlyThrLeuGlyIleVal**
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'SEQUENCE TYPE: amino acid
SEQUENCE LENGTH: 9 amino acids

45 **GlyThrLeuGlyIleValCysProIle**
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50 SEQ ID NO:20
SEQUENCE TYPE: amino acid
SEQUENCE LENGTH: 9 amino acids

55 **ThrLeuGlyIleValAlaProIleCys**
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SEQ ID NO:21
SEQUENCE TYPE: amino acid
SEQUENCE LENGTH: 9 amino acids

5 **LysLeuProAspLeuCysThrGluLeu**
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SEQ ID NO:22
SEQUENCE TYPE: amino acid
SEQUENCE LENGTH: 9 amino acids

10 **SerLeuGlnAspIleGluIleThrCys**
 1 5 9

SEQ ID NO:23
SEQUENCE TYPE: amino acid
SEQUENCE LENGTH: 9 amino acids

15 **LeuGlnAspIleGluIleThrCysVal**
 1 5 9

20 SEQ ID NO:24
SEQUENCE TYPE: amino acid
SEQUENCE LENGTH: 9 amino acids

25 **GluIleThrCysValTyrCysLysThr**
 1 5 9

30 SEQ ID NO:25
SEQUENCE TYPE: amino acid
SEQUENCE LENGTH: 9 amino acids

35 **LysThrValLeuGluLeuThrGluVal**
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40 SEQ ID NO:26
SEQUENCE TYPE: amino acid
SEQUENCE LENGTH: 9 amino acids

45 **GluLeuThrGluValPheGluPheAla**
 1 5 9

50 SEQ ID NO:27
SEQUENCE TYPE: amino acid
SEQUENCE LENGTH: 9 amino acids

55 **PheAlaPheLysAspLeuPheValVal**
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SEQ ID NO:28
SEQUENCE TYPE: amino acid
SEQUENCE LENGTH: 9 amino acids

AspThrLeuGluLysLeuThrAsnThr
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5 SEQ ID NO:29
SEQUENCE TYPE: amino acid
SEQUENCE LENGTH: 9 amino acids

10 LeuThrAsnThrGlyLeuTyrAsnLeu
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SEQ ID NO:30
SEQUENCE TYPE: amino acid
15 SEQUENCE LENGTH: 9 amino acids

20 ThrLeuGlnAspIleValLeuHisLeu
1 5 9

SEQ ID NO:31
SEQUENCE TYPE: amino acid
SEQUENCE LENGTH: 9 amino acids

25 PheGlnGlnLeuPheLeuAsnThrLeu
1 5 9

30 SEQ ID NO:32
SEQUENCE TYPE: amino acid
SEQUENCE LENGTH: 9 amino acids

35 GlnLeuPheLeuAsnThrLeuSerPhe
1 5 9

40 SEQ ID NO:33
SEQUENCE TYPE: amino acid
SEQUENCE LENGTH: 9 amino acids

LeuPheLeuAsnThrLeuSerPheVal
1 5 . 9

45 SEQ ID NO:34
SEQUENCE TYPE: amino acid
SEQUENCE LENGTH: 9 amino acids

50 LeuSerPheValCysProTrpCysAla
1 5 9

55 SEQ ID NO:35
SEQUENCE TYPE: amino acid
SEQUENCE LENGTH: 9 amino acids

5 **TyrArgAspGlyAsnProTyrAlaVal**
 1 5 9

5 SEQ ID NO:36
SEQUENCE TYPE: amino acid
SEQUENCE LENGTH: 9 amino acids

10 **TrpThrGlyArgCysMetSerCysCys**
 1 5 9

15 SEQ ID NO:37
'SEQUENCE TYPE: amino acid
SEQUENCE LENGTH: 9 amino acids

20 **MetSerCysCysArgSerSerArgThr**
 1 5 9

25 SEQ ID NO:38
SEQUENCE TYPE: amino acid
SEQUENCE LENGTH: 9 amino acids

30 **ThrThrAspLeuTyrCysTyrGluGln**
 1 5 9

35 SEQ ID NO:39
SEQUENCE TYPE: amino acid
SEQUENCE LENGTH: 9 amino acids

40 **GluIleAspGlyProAlaGlyGlnAla**
 1 5 9

45 SEQ ID NO:40
SEQUENCE TYPE: amino acid
SEQUENCE LENGTH: 9 amino acids

50 **HisValAspIleArgThrLeuGluAsp**
 1 5 9

55 SEQ ID NO:41
SEQUENCE TYPE: amino acid
SEQUENCE LENGTH: 9 amino acids

50 **IleIleLeuGluCysValTyrCysLys**
 1 5 9

55 SEQ ID NO:42
SEQUENCE TYPE: amino acid
SEQUENCE LENGTH: 9 amino acids

5 **ValTyrCysLysGlnGlnLeuLeuArg**
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SEQ ID NO:43
SEQUENCE TYPE: amino acid
SEQUENCE LENGTH: 9 amino acids

10 **GlnGlnLeuLeuArgArgGluValTyr**
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SEQ ID NO:44
SEQUENCE TYPE: amino acid
SEQUENCE LENGTH: 9 amino acids

15 **IleValTyrArgAspGlyAsnProTyr**
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20 SEQ ID NO:45
SEQUENCE TYPE: amino acid
SEQUENCE LENGTH: 9 amino acids

25 **TyrAlaValCysAspLysCysLeuLys**
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30 SEQ ID NO:46
SEQUENCE TYPE: amino acid
SEQUENCE LENGTH: 9 amino acids

35 **AlaValCysAspLysCysLeuLysPhe**
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40 SEQ ID NO:47
SEQUENCE TYPE: amino acid
SEQUENCE LENGTH: 9 amino acids

45 **ValCysAspLysCysLeuLysPheTyr**
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50 SEQ ID NO:48
SEQUENCE TYPE: amino acid
SEQUENCE LENGTH: 9 amino acids

55 **LysPheTyrSerLysIleSerGluTyr**
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SEQ ID NO:49
SEQUENCE TYPE: amino acid
SEQUENCE LENGTH: 9 amino acids

5 IleSerGluTyrArgHisTyrCysTyr
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SEQ ID NO:50
SEQUENCE TYPE: amino acid
SEQUENCE LENGTH: 9 amino acids

10 ArgHisTyrCysTyrSerLeuTyrGly
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SEQUENCE TYPE: amino acid
SEQUENCE LENGTH: 9 amino acids

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20 SEQ ID NO:52
SEQUENCE TYPE: amino acid
SEQUENCE LENGTH: 9 amino acids

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30 SEQ ID NO:53
SEQUENCE TYPE: amino acid
SEQUENCE LENGTH: 9 amino acids

35 GlnGlnTyrAsnLysProLeuCysAsp
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40 SEQ ID NO:54
SEQUENCE TYPE: amino acid
SEQUENCE LENGTH: 9 amino acids

45 LeuIleArgCysIleAsnCysGlnLys
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50 SEQ ID NO:55
SEQUENCE TYPE: amino acid
SEQUENCE LENGTH: 9 amino acids

55 HisLeuAspLysLysGlnArgPheHis
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SEQ ID NO:56
SEQUENCE TYPE: amino acid
SEQUENCE LENGTH: 9 amino acids

CysMetSerCysCysArgSerSerArg
1 5 9

5 SEQ ID NO:57
SEQUENCE TYPE: amino acid
SEQUENCE LENGTH: 9 amino acids

SerCysCysArgSerSerArgThrArg
1 5 9

10 SEQ ID NO:58
SEQUENCE TYPE: amino acid
15 SEQUENCE LENGTH: 9 amino acids

CysCysArgSerSerArgThrArgArg
1 5 9

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SEQUENCE TYPE: amino acid
SEQUENCE LENGTH: 9 amino acids

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30 SEQUENCE TYPE: amino acid
SEQUENCE LENGTH: 9 amino acids

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35 SEQ ID NO:61
SEQUENCE TYPE: amino acid
SEQUENCE LENGTH: 9 amino acids

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40 SEQ ID NO:62
45 SEQUENCE TYPE: amino acid
SEQUENCE LENGTH: 9 amino acids

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50 SEQ ID NO:63
SEQUENCE TYPE: amino acid
55 SEQUENCE LENGTH: 9 amino acids

ThrGlyArgCysMetSerCysCysArg
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5 SEQ ID NO:64
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 SEQUENCE LENGTH: 9 amino acids

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 SEQUENCE TYPE: amino acid
 15 SEQUENCE LENGTH: 9 amino acids

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 SEQUENCE TYPE: amino acid
 SEQUENCE LENGTH: 9 amino acids

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 30 SEQUENCE TYPE: amino acid
 SEQUENCE LENGTH: 9 amino acids

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 SEQUENCE TYPE: amino acid
 SEQUENCE LENGTH: 9 amino acids

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 SEQUENCE TYPE: amino acid
 SEQUENCE LENGTH: 9 amino acids

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 SEQUENCE TYPE: amino acid
 55 SEQUENCE LENGTH: 9 amino acids

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5 SEQ ID NO:71
SEQUENCE TYPE: amino acid
SEQUENCE LENGTH: 9 amino acids

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15 SEQUENCE LENGTH: 9 amino acids

CysTyrSerLeuTyrGlyThrThrLeu
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SEQUENCE TYPE: amino acid
SEQUENCE LENGTH: 9 amino acids

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1 5 9

25 SEQ ID NO:74
30 SEQUENCE TYPE: amino acid
SEQUENCE LENGTH: 9 amino acids

ArgAlaHisTyrAsnIleValThrPhe
1 5 9

Claims

- 40 1. A peptide with an amino acid sequence derived from a protein of human papilloma virus (HPV), wherein said peptide has the ability to bind to a human Major Histocompatibility complex (MHC) Class I molecule.
- 45 2. A peptide according to claim 1, wherein said amino acid sequence is derived from protein E6 or E7 of HPV16.
- 45 3. A peptide according to claim 1, wherein said amino acid sequence is derived from protein E6 or E7 of HPV18.
- 50 4. A peptide according to claim 1 or claim 2 or claim 3, wherein said amino acid sequence has the ability to bind to human MHC Class I allele HLA-A2.1.
- 50 5. A peptide according to claim 1, containing an amino acid sequence derived from protein E6 or E7 of HPV16, wherein said amino acid sequence has the ability to bind to human MHC Class I allele HLA-A2.1 and is selected from the group consisting of:

55	<table border="1" style="width: 100%; border-collapse: collapse;"> <tr> <td style="padding: 2px;">AMFQDPQER</td><td style="padding: 2px;">(residues 7- 15 of HPV16 protein E6)</td></tr> <tr> <td style="padding: 2px;">KLPQLCTEL</td><td style="padding: 2px;">(residues 18- 26 of HPV16 protein E6)</td></tr> <tr> <td style="padding: 2px;">QLCTELQTT</td><td style="padding: 2px;">(residues 21- 29 of HPV16 protein E6)</td></tr> <tr> <td style="padding: 2px;">LCTELQTTI</td><td style="padding: 2px;">(residues 22- 30 of HPV16 protein E6)</td></tr> </table>	AMFQDPQER	(residues 7- 15 of HPV16 protein E6)	KLPQLCTEL	(residues 18- 26 of HPV16 protein E6)	QLCTELQTT	(residues 21- 29 of HPV16 protein E6)	LCTELQTTI	(residues 22- 30 of HPV16 protein E6)
AMFQDPQER	(residues 7- 15 of HPV16 protein E6)								
KLPQLCTEL	(residues 18- 26 of HPV16 protein E6)								
QLCTELQTT	(residues 21- 29 of HPV16 protein E6)								
LCTELQTTI	(residues 22- 30 of HPV16 protein E6)								

(continued)

5	ELQTTIHDI LQTTIHDI TIHDIILEC IHDIIILECV CVYCKQQLL FAFRDLCIV KISEYRHYC PLCDLLIRC TLHEYMLDL YMLDLQPETT MLDLQPETT RLCVQSTHV TLEDLIMGT LLMGTGLIV	(residues 25- 33 of HPV16 protein E6) (residues 26- 34 of HPV16 protein E6) (residues 29- 37 of HPV16 protein E6) (residues 30- 38 of HPV16 protein E6) (residues 37- 45 of HPV16 protein E6) (residues 52- 60 of HPV16 protein E6) (residues 79- 87 of HPV16 protein E6) (residues 102-110 of HPV16 protein E6) (residues 7- 15 of HPV16 protein E7) (residues 11- 19 of HPV16 protein E7) (residues 12- 20 of HPV16 protein E7) (residues 66- 74 of HPV16 protein E7) (residues 78- 86 of HPV16 protein E7) (residues 82- 90 of HPV16 protein E7),
10		
15		

20 and a fragment, homolog, isoform, derivative, genetic variant or conservative variant of any one of these amino acid sequences which has the ability to bind to human MHC Class I allele HLA-A2.1.

- 25 6. A peptide according to claim 1, comprising an amino acid sequence derived from protein E6 or e7 of HPV18, wherein said amino acid sequence has the ability to bind to human MHC Class I allele HLA-A2.1 and is selected from the group consisting of:

30	KLPDLCTEL SLQDIEITC LQDIEITCV EITCVYCKT KTVLELTEV ELTEVFEFA FAFKDLFW DTLEKLTNT LTNTGLYNL TLQDIVLHL FQQLFLNLT QLFLNTLSF LFLNTLSFV LSFVCWPWCA	(residues 13- 21 of HPV18 protein E6) (residues 24- 32 of HPV18 protein E6) (residues 25- 33 of HPV18 protein E6) (residues 29- 37 of HPV18 protein E6) (residues 36- 44 of HPV18 protein E6) (residues 40- 48 of HPV18 protein E6) (residues 47- 55 of HPV18 protein E6) (residues 88- 96 of HPV18 protein E6) (residues 93-101 of HPV18 protein E6) (residues 7- 15 of HPV18 protein E7) (residues 86- 94 of HPV18 protein E7) (residues 88- 96 of HPV18 protein E7) (residues 89- 97 of HPV18 protein E7) (residues 94-102 of HPV18 protein E7),
35		
40		

45 and a fragment, homolog, isoform, derivative, genetic variant or conservative variant of any one of these amino acid sequences which has the ability to bind to human MHC Class I allele HLA-A2.1.

- 45 7. A peptide according to claim 1, wherein said amino acid sequence which has the ability to bind to human MHC Class I allele HLA-A1.
- 50 8. A peptide according to claim 1, comprising an amino acid sequence derived from protein E6 or E7 of HPV16, wherein said amino acid sequence has the ability to bind to human MHC Class I allele HLA-A1 and is selected from the group consisting of:

55	YRDGNPYAV WTGRCMSCC MSCCRSSRT TTDLYCYEQ EIDGPAGQA	(residues 61- 69 of HPV16 protein E6) (residues 139-147 of HPV16 protein E6) (residues 144-152 of HPV16 protein E6) (residues 19- 27 of HPV16 protein E7) (residues 37- 45 of HPV16 protein E7)
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(continued)

HVDIRTLED	(residues 73- 81 of HPV16 protein E7,
-----------	---------------------------------------

5 and a fragment, homolog, isoform, derivative, genetic variant or conservative variant of any one of these amino acid sequences which has the ability to bind to human MHC Class I allele HLA-A1.

9. A peptide according to claim 1, wherein said amino acid sequence has the ability to bind to human MHC Class I allele HLA-A3.2.

10. A peptide according to claim 1, comprising an amino acid sequence derived from protein E6 or E7 of HPV16, wherein said amino acid sequence has the ability to bind to human MHC Class I allele HLA-A3.2 and is selected from the group consisting of:

15	AMFQDPQER IILECVYCK CVYCKQQLL VYCKQQLLR QQLLRREVY IVYRDGNPY YAVCDKCLK AVCDKCLKF VCDKCLKFY KFYSKISEY KISEYRHYC ISEYRHYCY RHYCYSLYG SLYGTTLEQ TTLEQQYNK QQYNKPLCD LIRCINCQK HLDKKQRFH CMSCCRSSLR SCCRSSRTRR CCRSSRTRR HYNIVTFCC YNIVTFCC CCKCDSTLR KCDSTRLRC	(residues 7- 15 of HPV16 protein E6) (residues 33- 41 of HPV16 protein E6) (residues 37- 45 of HPV16 protein E6) (residues 38- 46 of HPV16 protein E6) (residues 42- 50 of HPV16 protein E6) (residues 59- 67 of HPV16 protein E6) (residues 67- 75 of HPV16 protein E6) (residues 68- 76 of HPV16 protein E6) (residues 69- 77 of HPV16 protein E6) (residues 75- 83 of HPV16 protein E6) (residues 79- 87 of HPV16 protein E6) (residues 80- 88 of HPV16 protein E6) (residues 84- 92 of HPV16 protein E6) (residues 89- 97 of HPV16 protein E6) (residues 93-101 of HPV16 protein E6) (residues 97-105 of HPV16 protein E6) (residues 107-115 of HPV16 protein E6) (residues 125-133 of HPV16 protein E6) (residues 143-151 of HPV16 protein E6) (residues 145-153 of HPV16 protein E6) (residues 146-154 of HPV16 protein E6) (residues 51- 59 of HPV16 protein E7) (residues 52- 60 of HPV16 protein E7) (residues 58- 66 of HPV16 protein E7) (residues 60- 68 of HPV16 protein E7),
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45 and a fragment, homolog, isoform, derivative, genetic variant or conservative variant of any one of these amino acid sequences which has the ability to bind to human MHC Class I allele HLA-A3.2.

46 11. A peptide according to claim 1, wherein said amino acid sequence has the ability to bind to human MHC Class I allele HLA-A11.2.

50 12. A peptide according to claim 1, comprising an amino acid sequence derived from protein E6 or E7 of HPV16, wherein said amino acid sequence has the ability to bind to human MHC Class I allele HLA-A11.2 and is selected from the group consisting of:

55	AMFQDPQER IILECVYCK CVYCKQQLL VYCKQQLLR	(residues 7- 15 of HPV16 protein E6) (residues 33- 41 of HPV16 protein E6) (residues 37- 45 of HPV16 protein E6) (residues 38- 46 of HPV16 protein E6)
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(continued)

5	QQLLRREVY IVYRDGNPY YAVCDKCLK AVCDKCLKF VCDKCLKFY KISEYRHYC ISEYRHHCY LIRCINCQK TGRCMSCCR CMSCCRSSR SCCRSSRTR HYNIVTFCC YNIVTFCCCK CCKCDSTLR	(residues 42- 50 of HPV16 protein E6) (residues 59- 67 of HPV16 protein E6) (residues 67- 75 of HPV16 protein E6) (residues 68- 76 of HPV16 protein E6) (residues 69- 77 of HPV16 protein E6) (residues 79- 87 of HPV16 protein E6) (residues 80- 88 of HPV16 protein E6) (residues 107-115 of HPV16 protein E6) (residues 140-148 of HPV16 protein E6) (residues 143-151 of HPV16 protein E6) (residues 145-153 of HPV16 protein E6) (residues 51- 59 of HPV16 protein E7) (residues 52- 60 of HPV16 protein E7) (residues 58- 66 of HPV16 protein E7),
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15		

20 and a fragment, homolog, isoform, derivative, genetic variant or conservative variant of any one of these amino acid sequences which has the ability to bind to human MHC Class I allele HLA-A11.2,

25 13. A peptide according to claim 1, wherein said amino acid sequence has the ability to bind to human MHC Class I allele HLA-A24.

30 14. A Peptide according to claim 1, comprising an amino acid sequence derivated from protein E6 or E7 of HPV16, wherein said amino acid sequence has the ability to bind to human MHC Class I allele HLA-A24 and is selected from the group consisting of:

35	MHQKRTAMF LQTTIHDI VYCKQQLLR LLRREVYDF VYDFAFRDL PYAVCDKCL KCLKFYSKI EYRHHCYSL HYCYSLYGT CYSLYGTTL RFHNIRGRW RAHYNIVTF	(residues 1- 9 of HPV16 protein E6) (residues 26- 34 of HPV16 protein E6) (residues 38- 46 of HPV16 protein E6) (residues 44- 52 of HPV16 protein E6) (residues 49- 57 of HPV16 protein E6) (residues 66- 74 of HPV16 protein E6) (residues 72- 80 of HPV16 protein E6) (residues 82- 90 of HPV16 protein E6) (residues 85- 93 of HPV16 protein E6) (residues 87- 95 of HPV16 protein E6) (residues 131-139 of HPV16 protein E6) (residues 49- 57 of HPV16 protein E7),
40		

45 and a fragment, homolog, isoform, derivative, genetic variant or conservative variant of any one of these amino acid sequences which has the ability to bind to human MHC Class I allele HLA-A24.

46 15. A peptide according to any one of the claims 1-14, having a length of from 9 to 12 amino acids.

50 16. A pharmaceutical composition containing a prophylactically or therapeutically effective amount of a peptide according to any one of the claims 1-15, and a pharmaceutically acceptable carrier, diluent, excipient or adjuvant.

55 17. A pharmaceutical composition containing a prophylactically or therapeutically effective amount of a peptide according to any one of the claims 1-15 which is able to induce a T cell response effective against HPV, and a pharmaceutically acceptable carrier, diluent, expient or adjuvant.

56 18. A pharmaceutical composition containing a prophylactically or therapeutically effective amount of a peptide according to any one of the claims 1-15 which is able to induce a HLA class I-restricted CD8+ cytotoxic T cell response effective against HPV, and a pharmaceutically acceptable carrier, diluent, excipient or adjuvant.

19. Use of a peptide having a sequence VCPICSQKP or GTLGIVCPI or TLGIVCPIC or a fragment, homolog, isoform, derivative, genetic variant or conservative variant thereof for the manufacture of a medicament for inducing an MHC-I mediated response.
- 5 20. Use of a peptide according to any one of claims 1-15, for the preparation of a medicament for prophylactically or therapeutically inducing in a human individual a HLA class I-restricted CD8+ cytotoxic T cell response effective against HPV.
- 10 21. Use of a peptide according to any one of claims 1-15 for preparing a pharmaceutical composition for prophylactically or therapeutically inducing in a human individual a HLA class I-restricted CD8+ cytotoxic T cell response effective against HPV.

Patentansprüche

- 15 1. Peptid mit einer Aminosäuresequenz, die von einem Protein des Humanpapillomvirus (HPV) abgeleitet ist, wobei das Peptid die Fähigkeit hat, an ein Molekül der Klasse I des humanen Haupthistokompatibilitätskomplexes (MHC) zu binden.
- 20 2. Peptid gemäß Anspruch 1, wobei die Aminosäuresequenz vom Protein E6 oder E7 des HPV16 abgeleitet ist.
3. Peptid gemäß Anspruch 1, wobei die Aminosäuresequenz vom Protein E6 oder E7 des HPV18 abgeleitet ist.
- 25 4. Peptid gemäß Anspruch 1 oder Anspruch 2 oder Anspruch 3, wobei die Aminosäuresequenz die Fähigkeit hat, an das humane MHC-Klasse-I-Allel HLA-A2.1 zu binden.
5. Peptid gemäß Anspruch 1, das eine Aminosäuresequenz enthält, die vom Protein E6 oder E7 des HPV16 abgeleitet ist, wobei die Aminosäuresequenz die Fähigkeit hat, an das humane MHC-Klasse-I-Allel HLA-A2.1 zu binden und aus der Gruppe ausgewählt ist, die aus folgenden besteht:

30	AMFQDPQER	(Reste 7-15 des HPV-16-Proteins E6)
	KLPQLCTEL	(Reste 18-26 des HPV-16-Proteins E6)
	QLCTELQTT	(Reste 21-29 des HPV-16-Proteins E6)
	LCTELQTTI	(Reste 22-30 des HPV-16-Proteins E6)
	ELQTTIHDI	(Reste 25-33 des HPV-16-Proteins E6)
	LQTTIHDI	(Reste 26-34 des HPV-16-Proteins E6)
	TIHDIILEC	(Reste 29-37 des HPV-16-Proteins E6)
	IHDIIILECV	(Reste 30-38 des HPV-16-Proteins E6)
35	CVYCKQQLL	(Reste 37-45 des HPV-16-Proteins E6)
	FAFRDLCIV	(Reste 52-60 des HPV-16-Proteins E6)
	KISEYRHYC	(Reste 79-87 des HPV-16-Proteins E6)
	PLCDLLIRC	(Reste 102-110 des HPV-16-Proteins E6)
40	TLHEYMLDL	(Reste 7-15 des HPV-16-Proteins E7)
	YMLDLQPET	(Reste 11-19 des HPV-16-Proteins E7)
	MLDLQPETT	(Reste 12-20 des HPV-16-Proteins E7)
	RLCVQSTHV	(Reste 66-74 des HPV-16-Proteins E7)
45	TLEDLIMGT	(Reste 78-86 des HPV-16-Proteins E7)
	LLMGTLGIV	(Reste 82-90 des HPV-16-Proteins E7)

sowie einem Fragment, Homologen, Isoform, Derivat, genetischen Variante oder konservativen Variante einer dieser Aminosäuresequenzen, das bzw. die die Fähigkeit hat, an das humane MHC-Klasse-I-Allel HLA-A2.1 zu binden.

- 55 6. Peptid gemäß Anspruch 1, das eine Aminosäuresequenz umfasst, die vom Protein E6 oder E7 des HPV18 abgeleitet ist, wobei die Aminosäuresequenz die Fähigkeit hat, an das humane MHC-Klasse-I-Allel HLA-A2.1 zu binden und aus der Gruppe ausgewählt ist, die aus folgenden besteht:

5	KLPDLCTEL SLQDIEITC LQDIEITCV EITCVYCKT KTVLELTEV ELTEVFEFA FAFKDLFVV	(Reste 13-21 des HPV-18-Proteins E6) (Reste 24-32 des HPV-18-Proteins E6) (Reste 25-33 des HPV-18-Proteins E6) (Reste 29-37 des HPV-18-Proteins E6) (Reste 36-44 des HPV-18-Proteins E6) (Reste 40-48 des HPV-18-Proteins E6) (Reste 47-55 des HPV-18-Proteins E6)
10	DTLEKLNT LTNTGLYNL TLQDIVLHL FQQQLFLNTL QLFLNLSF LFLNLSFV LSFVCPWCA	(Reste 88-96 des HPV-18-Proteins E6) (Reste 93-101 des HPV-18-Proteins E6) (Reste 7-15 des HPV-18-Proteins E7) (Reste 86-94 des HPV-18-Proteins E7) (Reste 88-96 des HPV-18-Proteins E7) (Reste 89-97 des HPV-18-Proteins E7) (Reste 94-102 des HPV-18-Proteins E7)
15		
20		sowie einem Fragment, Homologen, Isoform, Derivat, genetischen Variante oder konservativen Variante einer dieser Aminosäuresequenzen, das bzw. die die Fähigkeit hat, an das humane MHC-Klasse-I-Alell HLA2.1 zu binden.

7. Peptid gemäß Anspruch 1, wobei die Aminosäuresequenz die Fähigkeit hat, an das humane MHC-Klasse-I-Alell HLA-A1 zu binden.
8. Peptid gemäß Anspruch 1, das eine Aminosäuresequenz umfasst, die vom Protein E6 oder E7 des HPV16 abgeleitet ist, wobei die Aminosäuresequenz die Fähigkeit hat, an das humane MHC-Klasse-I-Alell HLA-A1 zu binden und aus der Gruppe ausgewählt ist, die aus folgenden besteht:

30	YRDGNPYAV WTGRCMSSC MSCCRSSLRT TTDLYCYEQ EIDGPAGQA HVDIRTLED	(Reste 61-69 des HPV-16-Proteins E6) (Reste 139-147 des HPV-16-Proteins E6) (Reste 144-152 des HPV-16-Proteins E6) (Reste 19-27 des HPV-16-Proteins E7) (Reste 37-45 des HPV-16-Proteins E7) (Reste 73-81 des HPV-16-Proteins E7)
35		

sowie einem Fragment, Homologen, Isoform, Derivat, genetischen Variante oder konservativen Variante einer dieser Aminosäuresequenzen, das bzw. die die Fähigkeit hat, an das humane MHC-Klasse-I-Alell HLA-A1 zu binden.

9. Peptid gemäß Anspruch 1, wobei die Aminosäuresequenz die Fähigkeit hat, an das humane MHC-Klasse-I-Alell HLA-A3.2 zu binden.
10. Peptid gemäß Anspruch 1, das eine Aminosäuresequenz umfasst, die vom Protein E6 oder E7 des HPV16 abgeleitet ist, wobei die Aminosäuresequenz die Fähigkeit hat, an das humane MHC-Klasse-I-Alell HLA-A3.2 zu binden und aus der Gruppe ausgewählt ist, die aus folgenden besteht:

50	AMFQDPQER IILECVYCK CVYCKQQLL VYCKQQLLR QQLLRREVY IVYRDNPY YAVCDKCLK AVCDKCLKF VCDKCLKFY	(Reste 7-15 des HPV-16-Proteins E6) (Reste 33-41 des HPV-16-Proteins E6) (Reste 37-45 des HPV-16-Proteins E6) (Reste 38-46 des HPV-16-Proteins E6) (Reste 42-50 des HPV-16-Proteins E6) (Reste 59-67 des HPV-16-Proteins E6) (Reste 67-75 des HPV-16-Proteins E6) (Reste 68-76 des HPV-16-Proteins E6) (Reste 69-77 des HPV-16-Proteins E6)
55		

(fortgesetzt)

5	KFYSKISEY KISEYRHYC ISEYRHHCY RHHCYSLYG SLYGTTLHQ TTLEQQYNK QQYNKPLCD LIRCINCQK HLDKKQRFH CMSCCRSSR SCCRSSRTR CCRSSRTRR HYNIVTFCC YNIVTFCC CCKCDSTLR KCDSTLRLC	(Reste 75-83 des HPV-16-Proteins E6) (Reste 79-87 des HPV-16-Proteins E6) (Reste 80-88 des HPV-16-Proteins E6) (Reste 84-92 des HPV-16-Proteins E6) (Reste 89-97 des HPV-16-Proteins E6) (Reste 93-101 des HPV-16-Proteins E6) (Reste 97-105 des HPV-16-Proteins E6) (Reste 107-115 des HPV-16-Proteins E6) (Reste 125-133 des HPV-16-Proteins E6) (Reste 143-151 des HPV-16-Proteins E6) (Reste 145-153 des HPV-16-Proteins E6) (Reste 146-154 des HPV-16-Proteins E6) (Reste 51-59 des HPV-16-Proteins E7) (Reste 52-60 des HPV-16-Proteins E7) (Reste 58-66 des HPV-16-Proteins E7) (Reste 60-68 des HPV-16-Proteins E7)
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sowie einem Fragment, Homologen, Isoform, Derivat, genetischen Variante oder konservativen Variante einer dieser Aminosäuresequenzen, das bzw. die die Fähigkeit hat, an das humane MHC-Klasse-I-Allel HLA-A3.2 zu binden.

25 11. Peptid gemäß Anspruch 1, wobei die Aminosäuresequenz die Fähigkeit hat, an das humane MHC-Klasse-I-Allel HLA-A11.2 zu binden.

30 12. Peptid gemäß Anspruch 1, das eine Aminosäuresequenz umfasst, die vom Protein E6 oder E7 des HPV16 abgeleitet ist, wobei die Aminosäuresequenz die Fähigkeit hat, an das humane MHC-Klasse-I-Allel HLA-A11.2 zu binden und aus der Gruppe ausgewählt ist, die aus folgenden besteht:

35	AMFQDPQER IILECVYCK CVYCKQQLL VYCKQQLLR QQLLRREVY IVYRDGNPY YAVCDKCLK AVCDKCLKF VCDKCLKFY KISEYRHYC ISEYRHHCY LIRCINCQK TGRCMSCCR CMSCCRSSR SCCRSSRTR HYNIVTFCC YNIVTFCC CCKCDSTLR	(Reste 7-15 des HPV-16-Proteins E6) (Reste 33-41 des HPV-16-Proteins E6) (Reste 37-45 des HPV-16-Proteins E6) (Reste 38-46 des HPV-16-Proteins E6) (Reste 42-50 des HPV-16-Proteins E6) (Reste 59-67 des HPV-16-Proteins E6) (Reste 67-75 des HPV-16-Proteins E6) (Reste 68-76 des HPV-16-Proteins E6) (Reste 69-77 des HPV-16-Proteins E6) (Reste 79-87 des HPV-16-Proteins E6) (Reste 80-88 des HPV-16-Proteins E6) (Reste 107-115 des HPV-16-Proteins E6) (Reste 140-148 des HPV-16-Proteins E6) (Reste 143-151 des HPV-16-Proteins E6) (Reste 145-153 des HPV-16-Proteins E6) (Reste 51-59 des HPV-16-Proteins E7) (Reste 52-60 des HPV-16-Proteins E7) (Reste 58-66 des HPV-16-Proteins E7)
40		
45		
50		

55 sowie einem Fragment, Homologen, Isoform, Derivat, genetischen Variante oder konservativen Variante einer dieser Aminosäuresequenzen, das bzw. die die Fähigkeit hat, an das humane MHC-Klasse-I-Allel HLA-A11.2 zu binden.

13. Peptid gemäß Anspruch 1, wobei die Aminosäuresequenz die Fähigkeit hat, an das humane MHC-Klasse-I-Allel

HLA-A24 zu binden.

- 5 14. Peptid gemäß Anspruch 1, das eine Aminosäuresequenz umfasst, die vom Protein E6 oder E7 des HPV16 abgeleitet ist, wobei die Aminosäuresequenz die Fähigkeit hat, an das humane MHC-Klasse-I-Allel HLA-A24 zu binden und aus der Gruppe ausgewählt ist, die aus folgenden besteht:

10	MHQKRTAMF LQTTIHDII VYCKQQLLR LLRREVYDF VYDFAFRDL PYAVCDKCL KCLKFYSKI EYRHHCYSL HYCYSLYGT CYSLYGTTL RFHNIRGRW RAHYNIVTF	(Reste 1-9 des HPV-16-Proteins E6) (Reste 26-34 des HPV-16-Proteins E6) (Reste 38-46 des HPV-16-Proteins E6) (Reste 44-52 des HPV-16-Proteins E6) (Reste 49-57 des HPV-16-Proteins E6) (Reste 66-74 des HPV-16-Proteins E6) (Reste 72-80 des HPV-16-Proteins E6) (Reste 82-90 des HPV-16-Proteins E6) (Reste 85-93 des HPV-16-Proteins E6) (Reste 87-95 des HPV-16-Proteins E6) (Reste 131-139 des HPV-16-Proteins E6) (Reste 49-57 des HPV-16-Proteins E7)
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20 sowie einem Fragment, Homologen, Isoform, Derivat, genetischen Variante oder konservativen Variante einer dieser Aminosäuresequenzen, das bzw. die die Fähigkeit hat, an das humane MHC-Klasse-I-Allel HLA-A24 zu binden.

- 25 15. Peptid gemäß einem der Ansprüche 1-14 mit einer Länge von 9 bis 12 Aminosäuren.
16. Pharmazeutische Zusammensetzung, die eine prophylaktisch oder therapeutisch wirksame Menge eines Peptids gemäß einem der Ansprüche 1-15 sowie einen pharmazeutisch annehmbaren Träger, Verdünnungsmittel, Exzipient oder Adjuvans enthält.
- 30 17. Pharmazeutische Zusammensetzung, die eine prophylaktisch oder therapeutisch wirksame Menge eines Peptids gemäß einem der Ansprüche 1-15, die in der Lage ist, eine gegen HPV wirksame T-Zell-Antwort zu induzieren, sowie einen pharmazeutisch annehmbaren Träger, Verdünnungsmittel, Exzipient oder Adjuvans enthält.
- 35 18. Pharmazeutische Zusammensetzung, die eine prophylaktisch oder therapeutisch wirksame Menge eines Peptids gemäß einem der Ansprüche 1-15, die in der Lage ist, eine gegen HPV wirksame Antwort von HLA-Klasse-I-beschränkten CD8-positiven cytotoxischen T-Zellen zu induzieren, sowie einen pharmazeutisch annehmbaren Träger, Verdünnungsmittel, Exzipient oder Adjuvans enthält.
- 40 19. Verwendung eines Peptids mit einer Sequenz VCPICSQKP oder GTLGIVCPI oder TLGIVCPIC oder eines Fragments, Homologen, Isoform, Derivats, genetischen Variante oder konservativen Variante davon zur Herstellung eines Medikaments zum Induzieren einer MHC-I-vermittelten Antwort.
- 45 20. Verwendung eines Peptids gemäß einem der Ansprüche 1-15 zur Herstellung eines Medikaments zum prophylaktischen oder therapeutischen Induzieren einer gegen HPV wirksamen Antwort von HLA-Klasse-I-beschränkten CD8-positiven cytotoxischen T-Zellen bei einem Menschen.
- 50 21. Verwendung eines Peptids gemäß einem der Ansprüche 1-15 zur Herstellung einer pharmazeutischen Zusammensetzung zum prophylaktischen oder therapeutischen Induzieren einer gegen HPV wirksamen Antwort von HLA-Klasse-I-beschränkten CD8-positiven cytotoxischen T-Zellen bei einem Menschen.

Revendications

- 55 1. Peptide ayant une séquence d'acides aminés dérivée d'une protéine du virus du papillome humain (HPV), où ledit peptide a la capacité de se lier à une molécule de classe I du complexe majeur d'histocompatibilité (CMH) humain.

2. Peptide selon la revendication 1, où ladite séquence d'acides aminés est dérivée de la protéine E6 ou E7 de HPV16.
3. Peptide selon la revendication 1, où ladite séquence d'acides aminés est dérivée de la protéine E6 ou E7 de HPV18.
- 5 4. Peptide selon la revendication 1 ou la revendication 2 ou la revendication 3, où ladite séquence d'acides aminés a la capacité de se lier à l'allèle HLA-A2.1 de classe I du CMH humain.
- 10 5. Peptide selon la revendication 1, contenant une séquence d'acides aminés dérivée de la protéine E6 ou E7 de HPV16, où ladite séquence d'acides aminés a la capacité de se lier à l'allèle HLA-A2.1 de classe I du CMH humain et est sélectionnée dans le groupe constitué par:

	AMFQDPQER	(résidus 7 - 15 de la protéine E6 de HPV16)
15	KLPQLCTEL	(résidus 18 - 26 de la protéine E6 de HPV16)
	QLCTELQTT	(résidus 21 - 29 de la protéine E6 de HPV16)
	LCTELQTTI	(résidus 22 - 30 de la protéine E6 de HPV16)
	ELQTTIHDI	(résidus 25 - 33 de la protéine E6 de HPV16)
	LQTTIHDI	(résidus 26 - 34 de la protéine E6 de HPV16)
20	TIHDIIILEC	(résidus 29 - 37 de la protéine E6 de HPV16)
	IHDIIILECV	(résidus 30 - 38 de la protéine E6 de HPV16)
	CVYCKQQLL	(résidus 37 - 45 de la protéine E6 de HPV16)
	FAPRDLCLIV	(résidus 52 - 60 de la protéine E6 de HPV16)
25	KISEYRHYC	(résidus 79 - 87 de la protéine E6 de HPV16)
	PLCDLLIRC	(résidus 102 - 110 de la protéine E6 de HPV16)
	TLHEYMLDL	(résidus 7 - 15 de la protéine E7 de HPV16)
	YMLDLQPET	(résidus 11 - 19 de la protéine E7 de HPV16)
	MLDLQPETT	(résidus 12 - 20 de la protéine E7 de HPV16)
30	RLCVQSTHV	(résidus 66 - 74 de la protéine E7 de HPV16)
	TLEDLIMGT	(résidus 78 - 86 de la protéine E7 de HPV16)
	LLMGTLGIV	(résidus 82 - 90 de la protéine E7 de HPV16)

et un fragment, homologue, isoforme, dérivé, variant génétique ou variant conservateur de l'une quelconque de ces séquences d'acides aminés qui a la capacité de se lier à l'allèle HLA-A2.1 de classe I du CMH humain.

- 35 6. Peptide selon la revendication 1, comprenant une séquence d'acides aminés dérivée de la protéine E6 ou E7 de HPV18, où ladite séquence d'acides aminés a la capacité de se lier à l'allèle HLA-A2.1 de classe I du CMH humain et est sélectionnée dans le groupe constitué par :

	KLPDLCTEL	(résidus 13 - 21 de la protéine E6 de HPV18)
40	SLQDIEITC	(résidus 24 - 32 de la protéine E6 de HPV18)
	LQDIEITCV	(résidus 25 - 33 de la protéine E6 de HPV18)
	EITCVYCKT	(résidus 29 - 37 de la protéine E6 de HPV18)
45	KTVLELTEV	(résidus 36 - 44 de la protéine E6 de HPV18)
	ELTEVFEFA	(résidus 40 - 48 de la protéine E6 de HPV18)
	FAFKDELFVV	(résidus 47 - 55 de la protéine E6 de HPV18)
	DTLEKLNTT	(résidus 88 - 96 de la protéine E6 de HPV18)
50	LTNTGLYNL	(résidus 93 - 101 de la protéine E6 de HPV18)
	TLQDIVLHL	(résidus 7 - 15 de la protéine E7 de HPV18)
	FQQLFLNLT	(résidus 86 - 94 de la protéine E7 de HPV18)
	QLFLNLSF	(résidus 88 - 96 de la protéine E7 de HPV18)
55	LFLNLSFV	(résidus 89 - 97 de la protéine E7 de HPV18)
	LSFVCPWCA	(résidus 94 - 102 de la protéine E7 de HPV18)

et un fragment, homologue, isoforme, dérivé, variant génétique ou variant conservateur de l'une quelconque de ces séquences d'acides aminés qui a la capacité de se lier à l'allèle HLA-A2.1 de classe I du CMH humain.

7. Peptide selon la revendication 1, où ladite séquence d'acides aminés a la capacité de se lier à l'allèle HLA-A1 de classe I du CMH humain.
- 5 8. Peptide selon la revendication 1, comprenant une séquence d'acides aminés dérivée de la protéine E6 ou E7 de HPV16, où ladite séquence d'acides aminés a la capacité de se lier à l'allèle HLA-A1 de classe I du CMH humain et est sélectionnée dans le groupe constitué par :

10	YRDGNPYAV WTGRCMSCC MSCCRSSLT TTDLYCYEQ EIDGPAGQQA HVDIRTLED	(résidus 61 - 69 de la protéine E6 de HPV16) (résidus 139 - 147 de la protéine E6 de HPV16) (résidus 144 - 152 de la protéine E6 de HPV16) (résidus 19 - 27 de la protéine E7 de HPV16) (résidus 37 - 45 de la protéine E7 de HPV16) (résidus 73 - 81 de la protéine E7 de HPV16)
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15 et un fragment, homologue, isoforme, dérivé, variant génétique ou variant conservateur de l'une quelconque de ces séquences d'acides aminés qui a la capacité de se lier à l'allèle HLA-A1 de classe I du CMH humain.

- 20 9. Peptide selon la revendication 1, où ladite séquence d'acides aminés a la capacité de se lier à l'allèle HLA-A3.2 de classe I du CMH humain.
10. Peptide selon la revendication 1, comprenant une séquence d'acides aminés dérivée de la protéine E6 ou E7 de HPV16, où ladite séquence d'acides aminés a la capacité de se lier à l'allèle HLA-A3.2 de classe I du CMH humain et est sélectionnée dans le groupe constitué par :

25	AMFQDPQER IILECVYCK CVYCKQQLL VYCKQQQLR QQLLRREVY IVYRDGNPY YAVCDKCLK AVCDKCLKF VCDKCLKFY KFYSKISEY KISEYRHYC ISEYRHHCY RHYCYSLYG SLYGTTLEQ TTLEQQYNIK QQYNKPLCD LIRCINCQK HLDKKQRFH CMSSCRSSR SCCRSSRTTR CCRSSRTTR HYNIVTFCC YNIVTFCC CCKCDSTLR KCDSTRLC	(résidus 7 - 15 de la protéine E6 de HPV16) (résidus 33 - 41 de la protéine E6 de HPV16) (résidus 37 - 45 de la protéine E6 de HPV16) (résidus 38 - 46 de la protéine E6 de HPV16) (résidus 42 - 50 de la protéine E6 de HPV16) (résidus 59 - 67 de la protéine E6 de HPV16) (résidus 67 - 75 de la protéine E6 de HPV16) (résidus 68 - 76 de la protéine E6 de HPV16) (résidus 69 - 77 de la protéine E6 de HPV16) (résidus 75 - 83 de la protéine E6 de HPV16) (résidus 79 - 87 de la protéine E6 de HPV16) (résidus 80 - 88 de la protéine E6 de HPV16) (résidus 84 - 92 de la protéine E6 de HPV16) (résidus 89 - 97 de la protéine E6 de HPV16) (résidus 93 - 101 de la protéine E6 de HPV16) (résidus 97 - 105 de la protéine E6 de HPV16) (résidus 107-115 de la protéine E6 de HPV16) (résidus 125 - 133 de la protéine E6 de HPV16) (résidus 143 - 151 de la protéine E6 de HPV16) (résidus 145 - 153 de la protéine E6 de HPV16) (résidus 146 - 154 de la protéine E6 de HPV16) (résidus 51 - 59 de la protéine E7 de HPV16) (résidus 52 - 60 de la protéine E7 de HPV16) (résidus 58 - 66 de la protéine E7 de HPV16) (résidus 60 - 68 de la protéine E7 de HPV16)
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55 et un fragment, homologue, isoforme, dérivé, variant génétique ou variant conservateur de l'une quelconque de ces séquences d'acides aminés qui a la capacité de se lier à l'allèle HLA-A3.2 de classe I du CMH humain.

11. Peptide selon la revendication 1, où ladite séquence d'acides aminés a la capacité de se lier à l'allèle HLA-A11.2

de classe I du CMH humain.

- 5 12. Peptide selon la revendication 1, comprenant une séquence d'acides aminés dérivée de la protéine E6 ou E7 de HPV16, où ladite séquence d'acides aminés a la capacité de se lier à l'allèle HLA-A11.2 de classe I du CMH humain et est sélectionnée dans le groupe constitué par :

	AMPQDPQER	(résidus 7 - 15 de la protéine E6 de HPV16)
10	IILECVYCK	(résidus 33 - 41 de la protéine E6 de HPV16)
	CVYCKQQLL	(résidus 37 - 45 de la protéine E6 de HPV16)
	VYCKQQQLR	(résidus 38 - 46 de la protéine E6 de HPV16)
	QQLLRREVY	(résidus 42 - 50 de la protéine E6 de HPV16)
15	IVYRDGNPY	(résidus 59 - 67 de la protéine E6 de HPV16)
	YAVCDKCLK	(résidus 67 - 75 de la protéine E6 de EIPV16)
	AVCDKCLKF	(résidus 68 - 76 de la protéine E6 de HPV16)
	VCDKCLKFY	(résidus 69 - 77 de la protéine E6 de HPV16)
	KISEYRHYC	(résidus 79 - 87 de la protéine E6 de HPV16)
20	ISEYRHHCY	(résidus 80 - 88 de la protéine E6 de HPV16)
	LIRCINCQK	(résidus 107 - 115 de la protéine E6 de HPV16)
	TGRCMSSCR	(résidus 140 - 148 de la protéine E6 de HPV16)
	CMSCCRSSL	(résidus 143 - 151 de la protéine E6 de HPV16)
	SCCRSSLTR	(résidus 145 - 153 de la protéine E6 de HPV16)
25	HYNIVTFCC	(résidus 51 - 59 de la protéine E7 de HPV16)
	YNIVTFCCK	(résidus 52 - 60 de la protéine E7 de HPV16)
	CCKCDSTLR	(résidus 58 - 66 de la protéine E7 de HPV16)

et un fragment, homologue, isoforme, dérivé, variant génétique ou variant conservateur de l'une quelconque de ces séquences d'acides aminés qui a la capacité de se lier à l'allèle HLA-A11.2 de classe I du CMH humain.

- 30 13. Peptide selon la revendication 1, où ladite séquence d'acides aminés a la capacité de se lier à l'allèle HLA-A24 de classe I du CMH humain.

- 35 14. Peptide selon la revendication 1, comprenant une séquence d'acides aminés dérivée de la protéine E6 ou E7 de HPV16, où ladite séquence d'acides aminés a la capacité de se lier à l'allèle HLA-A24 de classe I du CMH humain et est sélectionnée dans le groupe constitué par :

	MHQKRTAMF	(résidus 1-9 de la protéine E6 de HPV16)
40	LQTTIHDII	(résidus 26 - 34 de la protéine E6 de HPV16)
	VYCKQQQLR	(résidus 38 - 46 de la protéine E6 de HPV16)
	LLRREVYDF	(résidus 44 - 52 de la protéine E6 de HPV16)
	VYDFAFRDL	(résidus 49 - 57 de la protéine E6 de HPV16)
	PYAVCDKCL	(résidus 66 - 74 de la protéine E6 de HPV16)
45	KCLKFYSKI	(résidus 72 - 80 de la protéine E6 de HPV16)
	EYRHHCYSL	(résidus 82 - 90 de la protéine E6 de HPV16)
	HYCYSLYGT	(résidus 85 - 93 de la protéine E6 de HPV16)
	CYSLYGTTL	(résidus 87 - 95 de la protéine E6 de HPV16)
	RFHNIRGRW	(résidus 131 - 139 de 1a protéine E6 de HPV16)
50	RAHYNIVTF	(résidus 49 - 57 de 1a protéine E7 de HPV16)

et un fragment, homologue, isoforme, dérivé, variant génétique ou variant conservateur de l'une quelconque de ces séquences d'acides aminés qui a la capacité de se lier à l'allèle HLA-A24 de classe I du CMH humain.

- 55 15. Peptide selon l'une quelconque des revendications 1 à 14, ayant une longueur de 9 à 12 acides aminés.

16. Composition pharmaceutique contenant une quantité prophylactiquement ou thérapeutiquement efficace d'un pep-

tide selon l'une quelconque des revendications 1 à 15, et un véhicule, diluant, excipient ou adjuvant pharmaceutiquement acceptable.

5 **17.** Composition pharmaceutique contenant une quantité prophylactiquement ou thérapeutiquement efficace d'un peptide selon l'une quelconque des revendications 1 à 15 qui est capable d'induire une réponse des cellules T efficace contre le HPV, et un véhicule, diluant, excipient ou adjuvant pharmaceutiquement acceptable.

10 **18.** Composition pharmaceutique contenant une quantité prophylactiquement ou thérapeutiquement efficace d'un peptide selon l'une quelconque des revendications 1 à 15, qui est capable d'induire une réponse des cellules T cyto-toxiques CD8+ limitée à la classe I de HLA efficace contre le HPV, et un véhicule, diluant, excipient ou adjuvant pharmaceutiquement acceptable.

15 **19.** Utilisation d'un peptide ayant une séquence VCPICSQKP ou GTLGIVCPI ou TLGIVCPIC ou un fragment, homologue, isoforme, dérivé, variant génétique ou variant conservateur de ce dernier pour la fabrication d'un médicament destiné à induire une réponse à médiation par CMH-L

20 **20.** Utilisation d'un peptide selon l'une quelconque des revendications 1 à 15 pour la préparation d'un médicament destiné à induire prophylactiquement ou thérapeutiquement chez un individu humain une réponse des cellules T cytotoxiques CD8+ limitée à la classe I de HLA efficace contre le HPV.

25 **21.** Utilisation d'un peptide selon l'une quelconque des revendications 1 à 15 pour la préparation d'une composition pharmaceutique destinée à induire prophylactiquement ou thérapeutiquement chez un individu humain une ré-pense des cellules T cytotoxiques CD8+ limitée à la classe I de HLA efficace contre le HPV.

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Binding of HPV16 E6/7 peptides to HLA-A2.1

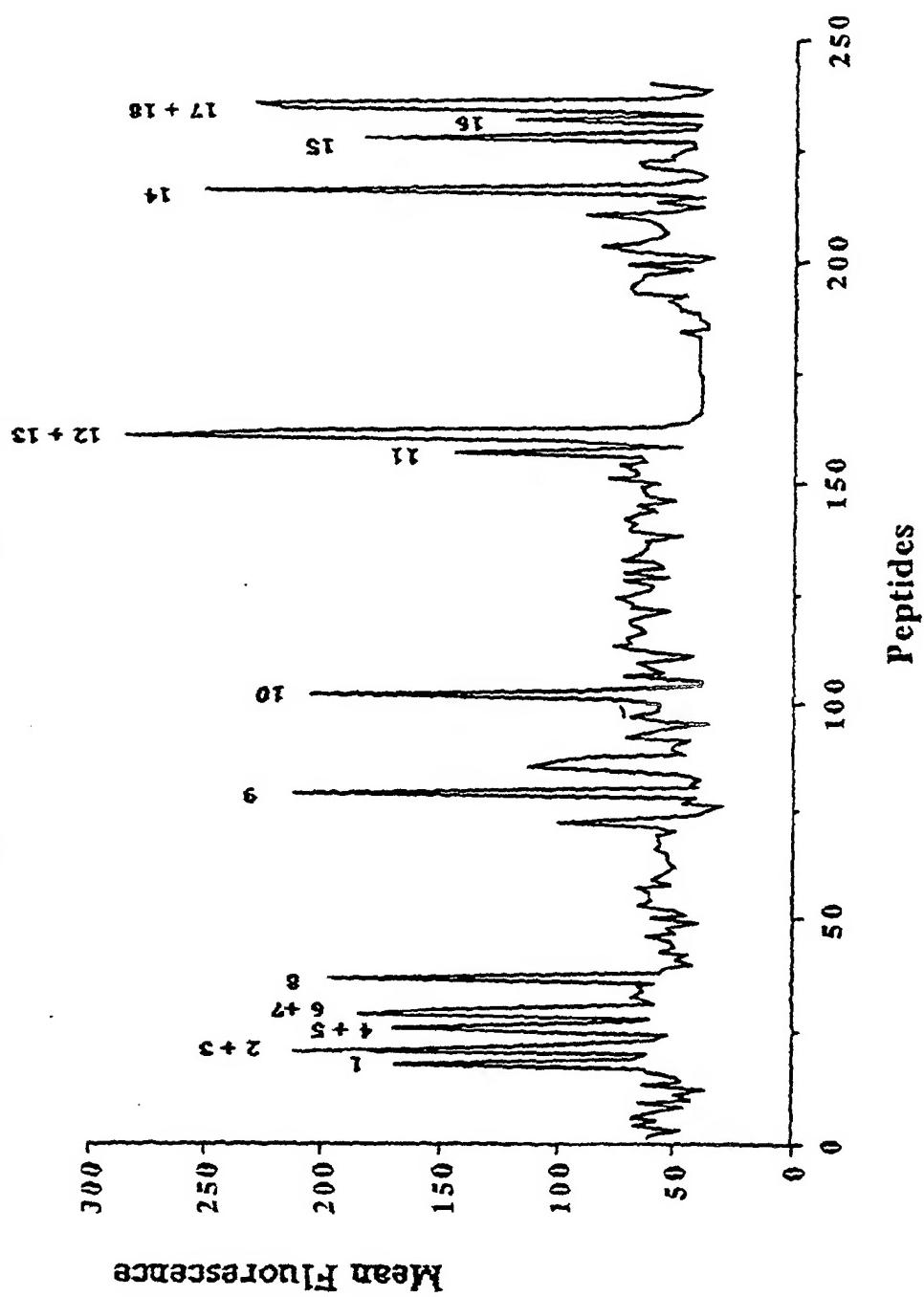


FIG. 1

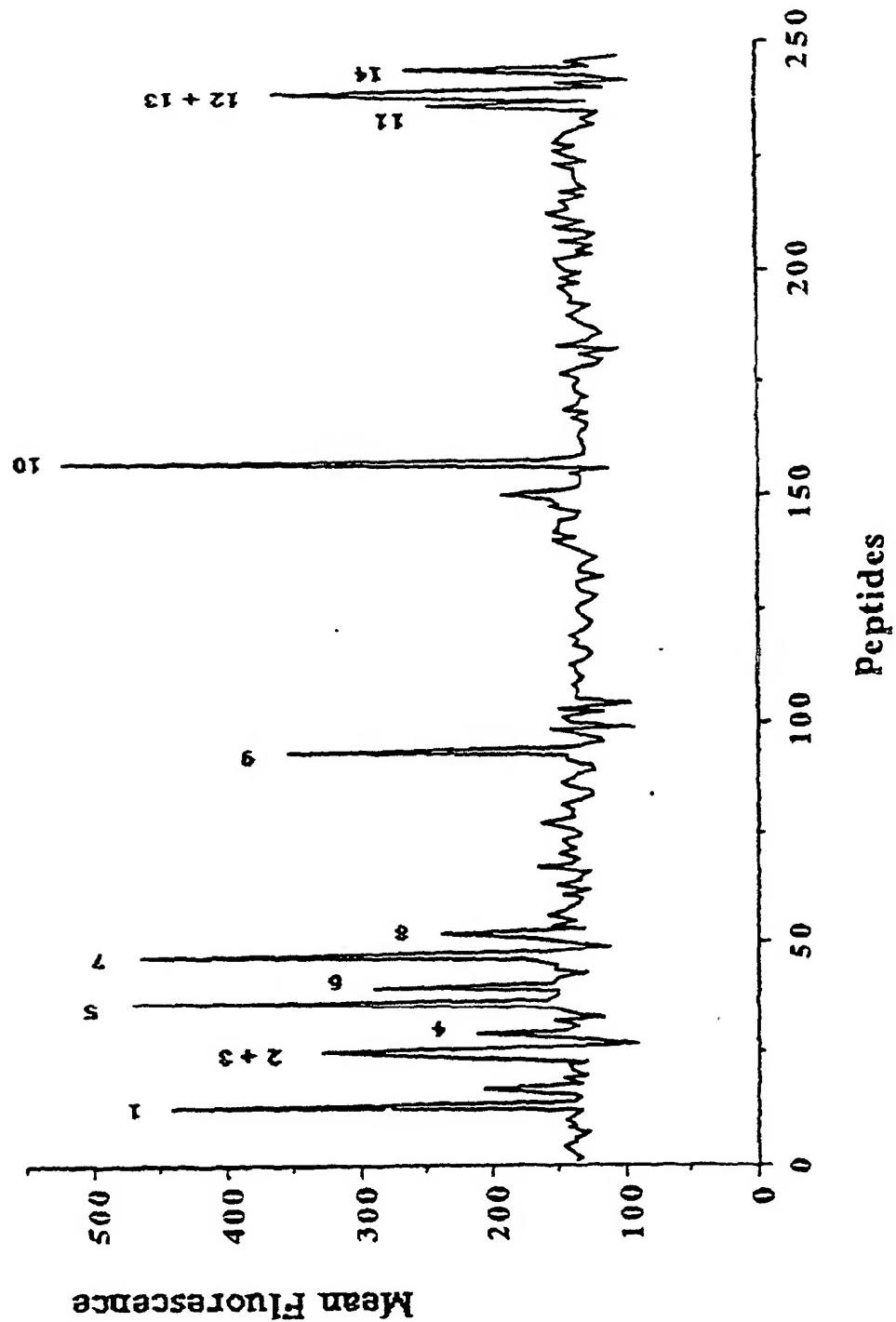
Binding of HPV18 E6/7 peptides to HLA- α 2.1

FIG. 2

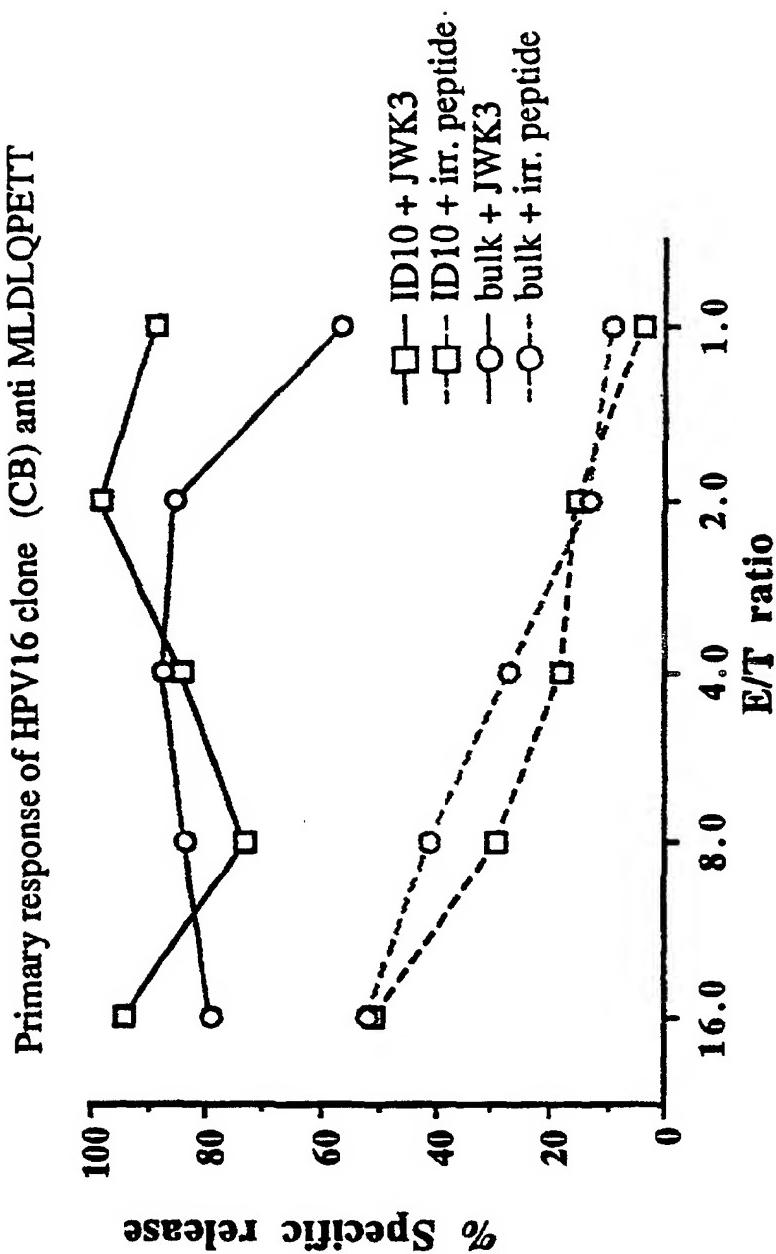


FIG. 3